

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run On: March 14, 2005, 17:14:02 ; Search time 1718 Seconds
(without alignments)

564.089 Million cell updates/sec

Title: US-10-672-399-10

Perfect score: 20

Sequence: 1 agggcgctctctgagtagcag 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hgt.*

3: gb_in.*

4: gb_on.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_to.*

11: gb_sts.*

12: gb_by.*

13: gb_un.*

14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	20	100.0	1581	6	CQ731079 Sequence
C 2	20	100.0	2088	9	U59269 Human hyalu
C 3	20	100.0	2108	9	D84424 Homo sapien
C 4	20	100.0	2116	6	AR220003 Sequence
C 5	20	100.0	2117	6	AR137038 Sequence
C 6	20	100.0	2119	9	BC035837 Homo sapi
C 7	20	100.0	193986	2	AC130783 Pan trogl
C 8	20	100.0	229155	9	AC018755 Homo sapi
C 9	18.4	92.0	517	4	AB017803 Bos tauru
C 10	17.4	87.0	600	11	BV099316 RPAMSEQO
C 11	17.4	87.0	600	11	BV160504 RPAMSEQO
C 12	17.4	87.0	2095	11	AB097568 Rattus no
C 13	17.4	87.0	2102	6	E13681 DNA encodin
C 14	17.4	87.0	2102	6	E28454 Hyaluronate
C 15	17.4	87.0	2102	6	E30971 Hyaluronon
C 16	17.4	87.0	2102	6	E34326 DNA for gen
C 17	17.4	87.0	2102	10	D82964 Mus musculu
C 18	17.4	87.0	2109	9	AY463695 Papio anu
C 19	17.4	87.0	72955	2	AC108651_3 Continuation (4 of

20	17.4	87.0	185623	2	AC137058
21	17.4	87.0	189862	2	AC108317
22	17.4	87.0	213263	10	AL593846 Mouse DNA
23	17.4	87.0	257325	2	AC116203 Rattus no
24	17.4	87.0	293184	2	AC079487 Mus muscu
25	16.8	84.0	278	6	AX898222 Sequence
26	16.8	84.0	278	6	BD033755 Sequence
27	16.8	84.0	313	6	AX886427 Sequence
28	16.8	84.0	313	6	BD026037 Sequence
29	16.8	84.0	465	9	AF367431 Homo sapi
30	16.8	84.0	529	9	AF367432 Homo sapi
31	16.8	84.0	536	9	AF367430 Homo sapi
32	16.8	84.0	555	11	BV037702 S212P6015
33	16.8	84.0	774	9	AF267852 Homo sapi
34	16.8	84.0	795	11	BV063966 S212P6739
35	16.8	84.0	3111	9	AK056640 Homo sapi
36	16.8	84.0	43859	9	AK006133 Homo sapi
37	16.8	84.0	45136	2	AC100349 Mus muscu
38	16.8	84.0	80065	2	AC016271 Homo sapi
39	16.8	84.0	110000	8	CR382131_11 Continuation (12 o
40	16.8	84.0	127109	9	AC106708 Homo sapi
41	16.8	84.0	128198	10	AL731701 Mouse DNA
42	16.8	84.0	141674	9	AC026671 Homo sapi
43	16.8	84.0	142447	10	AL627204 Mouse DNA
44	16.8	84.0	144791	2	AC142379 Rattus no
45	16.8	84.0	149727	2	AC073808 Mus muscu
46	16.8	84.0	150010	9	AC104782 Homo sapi
47	16.8	84.0	150354	2	AC133622 Rattus no
48	16.8	84.0	155211	2	AC019258 Homo sapi
49	16.8	84.0	159431	10	AC128702 Mus muscu
50	16.8	84.0	160872	2	AC053534 Homo sapi
51	16.8	84.0	172790	2	AC024165 Homo sapi
52	16.8	84.0	173643	2	AC119743 Homo sapi
53	16.8	84.0	174217	2	AC021408 Homo sapi
54	16.8	84.0	180816	2	AC110395 Rattus no
55	16.8	84.0	182700	2	AC145747 Mus muscu
56	16.8	84.0	183759	2	AC010935 Homo sapi
57	16.8	84.0	183865	2	AC130434 Homo sapi
58	16.8	84.0	191093	10	AL671765 Mouse DNA
59	16.8	84.0	192663	10	AC134406 Mus muscu
60	16.8	84.0	194366	10	AC109610 Mus muscu
61	16.8	84.0	194454	2	AC012357 Homo sapi
62	16.8	84.0	206321	2	AC124131 Mus muscu
63	16.8	84.0	206677	10	AC129085 Mus muscu
64	16.8	84.0	210172	2	AC121646 Rattus no
65	16.8	84.0	210928	2	AC118097 Rattus no
66	16.8	84.0	214436	2	AC119510 Rattus no
67	16.8	84.0	216139	2	AC132676 Rattus no
68	16.8	84.0	217943	2	AC127046 Rattus no
69	16.8	84.0	218698	9	AC007126 Homo sapi
70	16.8	84.0	220766	2	AC103203 Rattus no
71	16.8	84.0	225007	2	AC110885 Mus muscu
72	16.8	84.0	225698	10	AC100212 Mus muscu
73	16.8	84.0	229118	2	AC114408 Mus muscu
74	16.8	84.0	230056	2	AC134124 Rattus no
75	16.8	84.0	230569	2	AC108250 Rattus no
76	16.8	84.0	236164	10	AC101205 Mus muscu
77	16.8	84.0	236344	10	AL583889 Mouse DNA
78	16.8	84.0	238608	2	AC095637 Rattus no
79	16.8	84.0	238999	2	AC128410 Rattus no
80	16.8	84.0	243704	2	AC099277 Rattus no
81	16.8	84.0	243981	2	AC111281 Rattus no
82	16.8	84.0	252612	2	AC111263 Rattus no
83	16.8	84.0	253057	2	AC115253 Rattus no
84	16.8	84.0	254197	2	AF389853 Mus muscu
85	16.8	84.0	258293	2	AC114379 Rattus no
86	16.8	84.0	259757	2	AC114379 Rattus no
87	16.8	84.0	268756	2	AC117345 Rattus no
88	16.8	84.0	276958	2	AC110636 Rattus no
89	16.4	82.0	300	6	BD128919 Human gen
90	16.4	82.0	452	6	BD129543 Human gen
91	16.4	82.0	1191	6	CQ724801 Sequence
92	16.4	82.0	1611	6	AX747569 Sequence

93	16.4	82.0	1611	9	AK092491	Homo sapi	AK092491 Homo sapi	C 166	16.4	82.0	241696	2	AC130558	Rattus no
94	16.4	82.0	2057	6	BD159624	Primer fo	BD159624 Primer fo	C 167	16.4	82.0	244577	2	AC129706	Rattus no
95	16.4	82.0	2057	6	AX882261	Sequence	AX882261 Sequence	C 168	16.4	82.0	246469	2	AC131647	Rattus no
96	16.4	82.0	2057	6	AX822756	Homo sapi	AX822756 Homo sapi	C 169	16.4	82.0	246805	2	AC127181	Rattus no
97	16.4	82.0	2250	6	AX840058	Sequence	AX840058 Sequence	C 170	16.4	82.0	249184	2	AC111666	Rattus no
98	16.4	82.0	2753	6	BD160551	Primer fo	BD160551 Primer fo	C 171	16.4	82.0	253188	2	AC127877	Rattus no
99	16.4	82.0	2753	6	AX883823	Sequence	AX883823 Sequence	C 172	16.4	82.0	254698	2	AC094849	Rattus no
100	16.4	82.0	2753	9	AK024284	Homo sapi	AK024284 Homo sapi	C 173	16.4	82.0	255541	2	AC097730	Rattus no
101	16.4	82.0	2801	9	BC003555	Homo sapi	BC003555 Homo sapi	C 174	16.4	82.0	256899	2	AC097413	Rattus no
102	16.4	82.0	15105	6	AX840062	Sequence	AX840062 Sequence	C 175	16.4	82.0	257097	2	AC096199	Rattus no
103	16.4	82.0	70720	2	AC027823	Homo sapi	AC027823 Homo sapi	C 176	16.4	82.0	260873	2	AC121675	Rattus no
104	16.4	82.0	83087	2	AC079509	Mus muscu	AC079509 Mus muscu	C 177	16.4	82.0	263052	2	AC099360	Rattus no
105	16.4	82.0	88087	2	AC110708	Rattus no	AC110708 Rattus no	C 178	16.4	82.0	263349	2	AC134358	Rattus no
C 106	16.4	82.0	89729	5	EX649321	Zebrafish	EX649321 Zebrafish	C 179	16.4	82.0	275989	2	AC105503	Rattus no
	16.4	82.0	107455	9	AL5123308	Human DNA	AL5123308 Human DNA	C 180	16.4	82.0	280575	2	AC117364	Rattus no
107	16.4	82.0	171978	10	AC125138	Mus muscu	AC125138 Mus muscu	C 181	16.4	82.0	293757	10	AC095491	Rattus no
108	16.4	82.0	144432	2	AF276983	Homo sapi	AF276983 Homo sapi	C 182	16.4	82.0	294494	2	AC098385	Rattus no
109	16.4	82.0	154542	2	AC079040	Mus muscu	AC079040 Mus muscu	C 183	16.4	82.0	297293	2	AC125863	Rattus no
110	16.4	82.0	163399	2	AC079860	Homo sapi	AC079860 Homo sapi	C 184	16.4	82.0	301888	2	AC094881	Rattus no
111	16.4	82.0	165453	2	AC121860	Mus muscu	AC121860 Mus muscu	C 185	16.4	82.0	304517	2	AC096282	Rattus no
112	16.4	82.0	168544	2	AC131134	Rattus no	AC131134 Rattus no	C 186	16.4	82.0	327883	2	EX571684	Rattus no
113	16.4	82.0	171978	10	AC125138	Mus muscu	AC125138 Mus muscu	C 187	16.4	82.0	336984	2	AC113635	Rattus no
114	16.4	82.0	173251	2	AC139823	Homo sapi	AC139823 Homo sapi	C 188	16.4	82.0	3384	9	HS2239330	Homo sapi
115	16.4	82.0	175883	9	AP000808	Homo sapi	AP000808 Homo sapi	C 189	16.4	80.0	63451	9	AL662886	Human DNA
C 116	16.4	82.0	176757	4	AC095025	Sus scrofa	AC095025 Sus scrofa	C 190	16.4	80.0	68997	9	AC092861	Homo sapi
	16.4	82.0	177689	10	AC116500	Mus muscu	AC116500 Mus muscu	C 191	16.4	80.0	84797	8	AC011661	Genomic s
C 118	16.4	82.0	178382	2	AC139481	Homo sapi	AC139481 Homo sapi	C 192	16.4	80.0	147009	2	AC084179	Homo sapi
C 119	16.4	82.0	180005	2	AC136070	Rattus no	AC136070 Rattus no	C 193	16.4	80.0	147009	2	AC022566	Homo sapi
120	16.4	82.0	182072	2	AC133183	Mus muscu	AC133183 Mus muscu	C 194	16.4	80.0	154472	2	AC022566	Homo sapi
121	16.4	82.0	182715	2	AC130031	Rattus no	AC130031 Rattus no	C 195	15.8	79.0	243812	2	AC118510	Rattus no
C 122	16.4	82.0	183005	10	AC132570	Mus muscu	AC132570 Mus muscu	C 200	15.8	79.0	779	8	BD220581	Human gen
C 123	16.4	82.0	184891	2	AC108326	Rattus no	AC108326 Rattus no	C 201	15.8	79.0	841	10	AF183962	Mus muscu
C 124	16.4	82.0	186759	9	AL645608	Human DNA	AL645608 Human DNA	C 202	15.8	79.0	946	10	AF463665	Mus muscu
125	16.4	82.0	186836	9	AC079340	Homo sapi	AC079340 Homo sapi	C 203	15.8	79.0	1094	8	AK111378	Oryza sat
C 126	16.4	82.0	186848	2	AC145556	Mus muscu	AC145556 Mus muscu	C 204	15.8	79.0	1177	8	AF500581	Capicarpa
C 127	16.4	82.0	190078	2	AC139289	Homo sapi	AC139289 Homo sapi	C 205	15.8	79.0	1505	8	AK059039	Oryza sat
128	16.4	82.0	190752	2	AC080159	Mus muscu	AC080159 Mus muscu	C 206	15.8	79.0	1598	10	BC062643	Mus muscu
129	16.4	82.0	194199	2	AC135287	Rattus no	AC135287 Rattus no	C 207	15.8	79.0	1864	5	AC232496	Synanceia
C 130	16.4	82.0	194931	10	AC125063	Mus muscu	AC125063 Mus muscu	C 208	15.8	79.0	1991	9	BC007698	Homo sapi
C 131	16.4	82.0	196127	2	AC132788	Rattus no	AC132788 Rattus no	C 209	15.8	79.0	2069	9	CQ850809	Sequence
132	16.4	82.0	196715	2	AC141600	Homo sapi	AC141600 Homo sapi	C 210	15.8	79.0	2069	9	AK127991	Homo sapi
C 133	16.4	82.0	198026	2	AC124730	Mus muscu	AC124730 Mus muscu	C 211	15.8	79.0	2220	14	HSV52K	Hepevirus
C 134	16.4	82.0	200491	2	AB107102	Homo sapi	AB107102 Homo sapi	C 212	15.8	79.0	2273	4	AF184968	Oryctolag
C 135	16.4	82.0	200702	2	AC130278	Mus muscu	AC130278 Mus muscu	C 213	15.8	79.0	2561	10	AF199491	Mus muscu
C 136	16.4	82.0	203291	2	AC124762	Mus muscu	AC124762 Mus muscu	C 214	15.8	79.0	2561	6	AR064012	Sequence
C 137	16.4	82.0	203788	2	AC105965	Mus muscu	AC105965 Mus muscu	C 215	15.8	79.0	2614	6	BD235630	Single ge
C 138	16.4	82.0	205893	2	AC115530	Rattus no	AC115530 Rattus no	C 216	15.8	79.0	2614	6	AR195063	Sequence
C 139	16.4	82.0	208868	2	AC115946	Mus muscu	AC115946 Mus muscu	C 217	15.8	79.0	2614	6	AR212272	Sequence
C 140	16.4	82.0	211552	2	AC141271	Homo sapi	AC141271 Homo sapi	C 218	15.8	79.0	2614	6	BD057048	A single
141	16.4	82.0	212610	2	AC143325	Homo sapi	AC143325 Homo sapi	C 219	15.8	79.0	3037	10	AF183960	Mus muscu
142	16.4	82.0	214441	5	EX088571	Zebrafish	EX088571 Zebrafish	C 220	15.8	79.0	3071	9	BC023615	Homo sapi
C 143	16.4	82.0	214809	2	AC132744	Rattus no	AC132744 Rattus no	C 221	15.8	79.0	4384	9	BC064486	Homo sapi
C 144	16.4	82.0	214868	2	AC139122	Rattus no	AC139122 Rattus no	C 222	15.8	79.0	4384	9	BC080560	Homo sapi
145	16.4	82.0	216381	10	AC120138	Mus muscu	AC120138 Mus muscu	C 223	15.8	79.0	4396	9	BC049838	Homo sapi
C 146	16.4	82.0	216763	2	AC145176	Coriilla g	AC145176 Coriilla g	C 224	15.8	79.0	4766	10	RNGDNPN1	Rattus norv
147	16.4	82.0	217860	10	AC123714	Mus muscu	AC123714 Mus muscu	C 225	15.8	79.0	5000	6	AR526834	Sequence
C 148	16.4	82.0	219181	2	AC141063	Homo sapi	AC141063 Homo sapi	C 226	15.8	79.0	5174	10	BC060688	Mus muscu
C 149	16.4	82.0	219359	10	AC110250	Mus muscu	AC110250 Mus muscu	C 227	15.8	79.0	5334	6	CQ721623	Sequence
C 150	16.4	82.0	222536	2	AC117919	Rattus no	AC117919 Rattus no	C 228	15.8	79.0	5823	9	AX053263	Sequence
151	16.4	82.0	225043	2	AC105657	Rattus no	AC105657 Rattus no	C 229	15.8	79.0	5823	9	AX053263	Sequence
C 152	16.4	82.0	225551	2	CR847561	Danio rer	CR847561 Danio rer	C 230	15.8	79.0	5896	10	AL929468	Mouse DNA
153	16.4	82.0	227211	2	AC139288	Homo sapi	AC139288 Homo sapi	C 231	15.8	79.0	7227	8	AY298951	Chlamydom
154	16.4	82.0	227904	2	AC127672	Rattus no	AC127672 Rattus no	C 232	15.8	79.0	10801	10	AF215896	Pseudomon
C 155	16.4	82.0	229277	2	AC106518	Rattus no	AC106518 Rattus no	C 233	15.8	79.0	11849	1	AE004500	Sinorhizo
156	16.4	82.0	229365	2	AC097286	Rattus no	AC097286 Rattus no	C 234	15.8	79.0	14289	1	AE007209	Sinorhizo
157	16.4	82.0	231295	2	AC114134	Rattus no	AC114134 Rattus no	C 235	15.8	79.0	15621	9	AC011652	Homo sapi
C 158	16.4	82.0	232538	2	AC106066	Rattus no	AC106066 Rattus no	C 236	15.8	79.0	41511	9	AC131391	Homo sapi
C 159	16.4	82.0	234413	2	AC115456	Rattus no	AC115456 Rattus no	C 237	15.8	79.0	43658	14	HSV3PRGEN	Herpesvirus
C 160	16.4	82.0	234651	2	AC125553	Rattus no	AC125553 Rattus no	C 238	15.8	79.0	53130	2	AC101066	Mus muscu
161	16.4	82.0	236159	2	AC112875	Rattus no	AC112875 Rattus no							
162	16.4	82.0	238624	2	AC095116	Rattus no	AC095116 Rattus no							
C 163	16.4	82.0	238751	2	AC110220	Mus muscu	AC110220 Mus muscu							
C 164	16.4	82.0	239394	2	AC097603	Rattus no	AC097603 Rattus no							
C 165	16.4	82.0	240453	2	AC097603	Rattus no	AC097603 Rattus no							

C 239	15.8	79.0	53795	6	AX695749	AX695749 Sequence	312	15.8	79.0	179390	10	AC122190	AC122190 Mus muscu
C 240	15.8	79.0	61004	2	BX927305	Continuation (4 of	313	15.8	79.0	179439	2	AC131897	AC131897 Oryctolag
C 241	15.8	79.0	66624	2	AC101520	Mus muscu	C 314	15.8	79.0	181054	2	AC149084	AC149084 Mus muscu
C 242	15.8	79.0	73465	9	HS256613	AL109748 Homo sapi	C 315	15.8	79.0	181731	2	CR792458	CR792458 Danio rer
C 243	15.8	79.0	75131	2	AC023022	AL135799 Homo sapi	C 316	15.8	79.0	182650	2	AC141092	AC141092 Rattus no
C 244	15.8	79.0	79389	2	AL135799	AL135799 Homo sapi	C 317	15.8	79.0	182809	10	AC135859	AC135859 Mus muscu
C 245	15.8	79.0	94319	9	AC112501	AL12501 Homo sapi	C 318	15.8	79.0	183051	2	AC120130	AC120130 Mus muscu
C 246	15.8	79.0	94258	9	AL353715	Human DNA	C 319	15.8	79.0	183187	9	BS000003	BS000003 Pan trogl
C 247	15.8	79.0	93431	9	HU095737	U95737 Human Chrom	C 320	15.8	79.0	183462	10	AC129315	AC129315 Mus muscu
C 248	15.8	79.0	93519	9	AC130458	AL130458 Homo sapi	C 321	15.8	79.0	184164	10	AC126944	AC126944 Mus muscu
C 249	15.8	79.0	103563	10	AL929313	AL929313 Mouse DNA	C 322	15.8	79.0	184194	9	AC011257	AC011257 Homo sapi
C 250	15.8	79.0	103826	9	AL139339	AL139339 Human DNA	C 323	15.8	79.0	184289	8	AP003545	AP003545 Oryza sat
C 251	15.8	79.0	106093	9	AC007561	AC007561 Homo sapi	C 324	15.8	79.0	185666	2	AC101747	AC101747 Mus muscu
C 252	15.8	79.0	106826	2	AC020829	Mus muscu	C 325	15.8	79.0	185871	2	AC109251	AC109251 Mus muscu
C 253	15.8	79.0	110000	1	AE000516	Continuation (5 of	C 326	15.8	79.0	186120	9	AC007598	AC007598 Homo sapi
C 254	15.8	79.0	110000	8	CR382131	Continuation (28 o	C 327	15.8	79.0	186347	2	AC107710	AC107710 Mus muscu
C 255	15.8	79.0	111934	9	AF281074	AF281074 Homo sapi	C 328	15.8	79.0	186431	10	AC113092	AC113092 Mus muscu
C 256	15.8	79.0	112544	9	AC109892	AC109892 Homo sapi	C 329	15.8	79.0	186517	9	AC022710	AC022710 Homo sapi
C 257	15.8	79.0	112930	14	HSGEND	X64346 Salmirline	C 330	15.8	79.0	190400	2	AC102726	AC102726 Mus muscu
C 258	15.8	79.0	113027	14	SHE410493	AF410493 Salmirline	C 331	15.8	79.0	190421	10	AC132419	AC132419 Mus muscu
C 259	15.8	79.0	113626	2	AC145363	AC145363 Dasytus n	C 332	15.8	79.0	190735	2	AC026084	AC026084 Homo sapi
C 260	15.8	79.0	114793	9	AF217796	AF217796 Homo sapi	C 333	15.8	79.0	191439	10	AL627302	AL627302 Mouse DNA
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C 265	15.8	79.0	135689	9	AC023755	AC023755 Homo sapi	C 338	15.8	79.0	197411	10	AC135961	AC135961 Mus muscu
C 266	15.8	79.0	135851	9	AC091714	AC091714 Papio anu	C 339	15.8	79.0	198294	10	AC135104	AC135104 Mus muscu
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C 268	15.8	79.0	141809	10	AC125012	AC125012 Mus muscu	C 341	15.8	79.0	199140	2	BX005251	BX005251 Mus muscu
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C 272	15.8	79.0	144037	2	RM484K6	AL603721 Rattus no	C 345	15.8	79.0	207275	2	AC130506	AC130506 Rattus no
C 273	15.8	79.0	152244	9	AP000352	AP000352 Homo sapi	C 346	15.8	79.0	207312	10	AC110530	AC110530 Mus muscu
C 274	15.8	79.0	153170	9	HS1103G7	AL034548 Human DNA	C 347	15.8	79.0	207424	10	AC090489	AC090489 Genomic s
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C 277	15.8	79.0	157219	2	BX000348	BX000348 Danio rer	C 350	15.8	79.0	212835	2	AC007612	AC007612 Homo sapi
C 278	15.8	79.0	157757	10	AC131189	AC131189 Mus muscu	C 351	15.8	79.0	213687	2	AC119257	AC119257 Mus muscu
C 279	15.8	79.0	157860	9	AL391241	AL391241 Human DNA	C 352	15.8	79.0	213980	2	AC138547	AC138547 Mus muscu
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C 290	15.8	79.0	168153	2	AC131519	AC131519 Rattus no	C 363	15.8	79.0	223729	2	AC079441	AC079441 Mus muscu
C 291	15.8	79.0	168337	2	AC118956	AC118956 Rattus no	C 364	15.8	79.0	223827	2	AC098771	AC098771 Rattus no
C 292	15.8	79.0	169465	10	AL606976	AL606976 Mouse DNA	C 365	15.8	79.0	225687	2	AC098771	AC098771 Rattus no
C 293	15.8	79.0	169536	2	AC016496	AC016496 Homo sapi	C 366	15.8	79.0	226348	2	AC151108	AC151108 Mus muscu
C 294	15.8	79.0	169838	10	AL713861	AL713861 Mouse DNA	C 367	15.8	79.0	226714	2	AC079532	AC079532 Mus muscu
C 295	15.8	79.0	170022	2	AC120072	AC120072 Rattus no	C 368	15.8	79.0	226736	10	AC098881	AC098881 Mus muscu
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C 299	15.8	79.0	171551	8	OSJN00177	AL662976 Oryza sat	C 372	15.8	79.0	231484	2	AC096379	AC096379 Rattus no
C 300	15.8	79.0	172380	10	AC132522	AC126252 Mus muscu	C 373	15.8	79.0	231767	2	AC094531	AC094531 Rattus no
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C 302	15.8	79.0	174373	9	AC132216	AC132216 Homo sapi	C 375	15.8	79.0	232945	2	AC103156	AC103156 Rattus no
C 303	15.8	79.0	174833	2	AC127686	AC127686 Mus muscu	C 376	15.8	79.0	233785	2	AC105715	AC105715 Rattus no
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C 308	15.8	79.0	178181	9	AC064868	AC064868 Homo sapi	C 381	15.8	79.0	236692	2	AC073773	AC073773 Mus muscu
C 309	15.8	79.0	178414	2	AC137801	AC137801 Homo sapi	C 382	15.8	79.0	238079	2	AC096000	AC096000 Rattus no
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C 311	15.8	79.0	179386	10	BX255910	BX255910 Mouse DNA	C 384	15.8	79.0	238877	2	AC115347	AC115347 Rattus no

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SOURCE	Homo sapiens					
ORGANISM	Homo sapiens					
REFERENCE	1					
AUTHORS	Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.					
TITLE	Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof					
JOURNAL	Patent: WO 02068579-A 17013 06-SEP-2002; PE Corporation (NY) (US)					
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RESULT 2
LOCUS HSU59269 2088 bp mRNA linear PRI 24-SEP-1996
DEFINITION Human hyaluronan synthase mRNA, complete cds.
ACCESSION U59269
VERSION U59269.1 GI:1556464
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2088)
AUTHORS Shyan,A.M., Heldin,P., Butcher,E.C., Yoshino,T. and Briskin,M.J.
TITLE Functional cloning of the cDNA for a human hyaluronan synthase
JOURNAL J. Biol. Chem. 271 (38), 23395-23399 (1996)
MEDLINE 96394438
PUBMED 8798544
REFERENCE 2 (bases 1 to 2088)
AUTHORS Briskin,M.J. and Shyjan,A.M.
TITLE Direct Submission
JOURNAL Submitted (24-MAY-1996) LeukoSite Inc., 215 First Street,
Cambridge, MA 02142, USA
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VSFSLSLRYWAFNVERACQSYFHCVSCISGPLGLYRNLLQGLEAWYKQFLGTHC
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WHRHRAWMTYEAUVVSGLPFPFVAATVLRFLYAGRPWALLWVLLCVGVAKAAAPAA
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DB 1134 AGGGCGTCTCTGAGTAGCAG 1115

RESULT 3
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DEFINITION Homo sapiens mRNA for hyaluronan synthase, complete cds.
ACCESSION D84424
VERSION D84424.1 GI:1401033
KEYWORDS hHAS; hyaluronan synthase.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2108)
AUTHORS Itano,N. and Kimata,K.
TITLE Molecular cloning of human hyaluronan synthase
JOURNAL Biochem. Biophys. Res. Commun. 222 (3), 816-820 (1996)
MEDLINE 96244584
PUBMED 8651928
REFERENCE 2 (bases 1 to 2108)
AUTHORS Itano,N.
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 2108)
AUTHORS Itano,N.
TITLE Direct Submission
JOURNAL Submitted (16-APR-1996) Naoki Itano, Aichi Medical University,
Institute for Molecular Science of Medicine; Nagakute, Aichi-gun,
Aichi 480-11, Japan (Tel:052-364-4811(ex.2087), Fax:0561-63-3532)
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/clone_lib="/lgtl1"
/dev_stage="fetal"
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/product="hyaluronan synthase"
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/db_xref="GI:1401034"
/translation="MTWYAAAGVPLASDRYGLLAFGLYGAFLSAHLVAQSLFAYLEHRR
RVAAAARGPLDAATARSVALTISAYQEDPAYLRQCLASARALLYPRARVRLMVVDGN
RAEDLYMDMFREVFADGDPATYVDNGYHPQWPAAGAVGAGAREVEADPGRLA
VEALVTRRCVCVCAORWGKREYMTAFKALGDSVDYVQVCDSDRLDPALLLELVRL
LDEDPRVGAVGGDVRILNPLDSWSVFSLSRLRYWAFNVERACQSYFHCVSCISGPLGL
YRNLLQGLEAWYKQFLGTHCTFGDDRHUTNRLSMGYATKYTSRSCYSETPSSFL
LRWLSSQTRWSKYFREWLYNALWHRHRAWMTYEAUVVSGLPFPFVAATVLRFLYAGR
PWALLWVLLCVGVAKAAAPAAWLRGCLRVLVLSYAPLYMCGLLPAKFLALVTMNSG
WTSGRRKRLAANYVPLPLALWALLLGLLVRSVAHEARADWSGPRAAEAYHLAAGAG
AYVGYVWVAMLTLYVWGVRLCRRRTGGYRVQV"
ORIGIN
Query Match      100.0%; Score 20; DB 9; Length 2108;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
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DB 1142 AGGGCGTCTCTGAGTAGCAG 1123

RESULT 4
LOCUS AR220003/c 2116 bp mRNA linear PAT 26-SEP-2002
DEFINITION Sequence 1 from patent US 6423514.
ACCESSION AR220003
VERSION AR220003.1 GI:23324403
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2116)
AUTHORS Briskin,M.J.
TITLE Mammalian hyaluronan synthases, nucleic acids and uses thereof
JOURNAL Patent: US 6423514-A 1 23-JUL-2002;
FEATURES
source
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/organism="unknown"
/mol_type="mRNA"
ORIGIN

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Qy 1 AGGCGCTCTGAGTAGCAG 20
Db 1137 AGGCGCTCTGAGTAGCAG 1118

RESULT 7
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LOCUS Pan troglodytes clone CH251-426A12, WORKING DRAFT SEQUENCE, 8
DEFINITION ordered pieces.
ACCESSION AC130783
VERSION AC130783.2 GI:25100968
KEYWORDS HTG; HTGS PHASE2; HTGS_DRAFT.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
REFERENCE 1 (bases 1 to 193986)
AUTHORS Akter,N., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Cariaga,K., Coleman,B., Engle,J., Granite,S., Guan,X., Gupta,J.,
Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Idol,J.R., Karlins,E.,
Laric,P., Lee-Lin,S.-Q., Legaspi,R., Maduro,Q.L., Maduro,V.B.,
Marques,E.H., Mastello,C., Maskeri,B., McDowell,J.,
Paguirigan,C., Pearson,R., Portnoy,M.E., Prasad,A.,
Reddix-Dugue,N., Schandler,K., Schueler,M.G., Sison,C.,
Stantripop,S., Thomas,J.W., Thomas,P.J., Touchman,J.W., Vogt,J.L.,
Wetherby,K.D., Wiggins,L., Young,A. and Green,E.D.
NISC Comparative Sequencing Initiative
Unpublished
NISC 2 (bases 1 to 193986)
AUTHORS Green,E.D.
TITLE Direct Submission
JOURNAL Submitted (14-AUG-2002) NIH Intramural Sequencing Center, 8717
Grosvmont Circle, Gaithersburg, MD 20877, USA
REFERENCE 3 (bases 1 to 193986)
AUTHORS Green,E.D.
TITLE Direct Submission
JOURNAL Submitted (19-NOV-2002) NIH Intramural Sequencing Center, 8717
Grosvmont Circle, Gaithersburg, MD 20877, USA
COMMENT On Nov 19, 2002 this sequence version replaced gi:22218453.
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc.zoo@nhgri.nih.gov
----- Project Information
Center project name: dxd
Center clone name: 426A12

The sequence data in this record represents an 'enhanced'
version of a Phase 2 submission. Specifically, the indicated
order and orientation of each sequence contig has been
established using one or more of the following: read-pair
data from individual subclones, overlaps with neighboring
clones, alignment with available reference sequence (e.g.,
human), and/or confirmation by PCR testing. In addition,
the sequence assembly is based on at least 8x average
coverage in Q20 bases and has been reviewed to rule out
gross misassemblies, the low-quality ends of sequence
contigs have been trimmed away, and each base is associated
with a Phrap-derived quality score.
----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 191764 bases at least Q40
Consensus quality: 192510 bases at least Q30
Consensus quality: 192998 bases at least Q20
Insert size: 184000; agarose-fp
Quality coverage: 11.49x in Q20 bases; agarose-fp
Quality coverage: 10.94x in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 11512: contig of 11512 bp in length
* 11513 11612: gap of unknown length
* 11613 59488: contig of 47876 bp in length
* 59489 59588: gap of unknown length
* 59589 103266: contig of 43678 bp in length
* 103267 103366: gap of unknown length
* 103367 127885: contig of 24519 bp in length
* 127886 127985: gap of unknown length
* 127986 129692: contig of 1707 bp in length
* 129693 129792: gap of unknown length
* 129793 131077: contig of 1285 bp in length
* 131078 131177: gap of unknown length
* 131178 174663: contig of 43486 bp in length
* 174664 174763: gap of unknown length
* 174764 193986: contig of 19223 bp in length.
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1..11512
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clone_end:SP6
vector_side:left
misc_feature
1..76
/note="clone overlaps with GenBank Accession Number
AC132069 clone CH251-132A6 (center project name dxc)"
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11613..59488
/note="assembly_fragment"
misc_feature
59589..103266
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misc_feature
103367..127885
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127886..129692
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129793..131077
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131178..174663
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misc_feature
174764..193986
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clone_end:T7
vector_side:right
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Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGGCGCTCTGAGTAGCAG 20
Db 128496 AGGCGCTCTGAGTAGCAG 128515
RESULT 8
AC018755
LOCUS AC018755 229155 bp DNA linear PRI 26-JUL-2000
DEFINITION Homo sapiens chromosome 19, BAC BC330783 (CIT-HSPC_470E3), complete
sequence.
ACCESSION AC018755
VERSION AC018755.3 GI:9454515

```

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KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 229155)
AUTHORS Lamerdin, J.E., McCreedy, P.M., Skowronski, E., Viswanathan, V.,
Burkhart-Schultz, K., Gordon, L., Dias, J., Ramirez, M., Stilwagen, S.,
Phan, H., Velasco, N., Do, L., Regala, N., Terry, A., Brower, A.,
Garnes, J., Danganan, L., Erlar, A., Christensen, M., Georgescu, A.,
Avila, J., Liu, S., Andreise, T., Trankheim, M., Attix, C.,
Amico-Keller, G., Coefield, J., Duarte, S., Lucas, S., Bruce, R.,
Thomas, P., Quan, G., Krommiller, B., Arellano, A., Sanders, C., Ow, D.,
Nolan, M., Trong, S., Kobayashi, A., Olsen, A.S. and Carrano, A.V.
Sequence analysis of a 5-Mb region in 19q13.4
Unpublished
JOURNAL 2 (bases 1 to 229155)
REFERENCE DOE Joint Genome Institute.
AUTHORS Direct Submission
TITLE Submitted (19-DEC-1999) Production Sequencing Facility, DOE Joint
JOURNAL Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 229155)
AUTHORS Lamerdin, J.E.
TITLE Direct Submission
JOURNAL Submitted (26-JUL-2000) DOE Joint Genome Institute, Lawrence
Livermore National Laboratory, Livermore, CA 94550
COMMENT On Jul 26, 2000 this sequence version replaced gi:7458780.
Map and sequence oriented from centromere to q-telomere. BC330783
(CIT-HSPC 470E3) is overlapped on the left by BC849408
(CITB-E1 3073N11, AC020914) from bases 1 to 125 of this accession,
and overlaps cosmid R28782 (LLNL-R 248F10, AC005946) on the right
from bases 217,905 to 229,155 of this accession. Additional
chromosome 19 map and sequence information may be obtained at:
http://www-bio.llnl.gov/bbrp/genome/genome.html.
FEATURES
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Location/Qualifiers
1..229155
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosomes="19"
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/clone="CTC-470E3 (LLNL clone name BC330783)"
/clone_lib="Caltech human BAC library C"
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Gene <299..16870
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DPAQRCLYRDVLMLEYLSHIFVAGYHIIPNPEVIFMLKEKEPRVEAEVSHQCRERF
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DIEQLDDVVGSQLFSHSSDACSKNIHTGETCKGNQCKVCGHKQSLKQHIHTQK
KPDGCEGSGFTQKHSHLFAQQRIHSVGNLHCCKGKAPFQMLSLFPHQTHREKLYE
CICKEGCVFIORSELTTHQRTKTRKXKCHDCGKAFQMLSLFPHQTHREKLYE
CEGQKGFQNSLTIIHQIHTGEQYACSECAFTKSTLSLHQRIHSGOKSYVCI
ECGQAFIOKALHIVHRSHTGEKPYCHNCGKSPISKSQLDIHRIHTGEKPYVCD
GTFTQKSHLHOKIHTGERHVCSECAFNKSIKSMHORIHTEKPYKCEGK
ATSKSQPKHQRIHTGEKPYVCTEGKAFNGSNPFHKQIHTHTRERPFVCKGKAP
VQSELTHTHRTMGKPYCELDGKSFSGKQKLVKQRIHTGERPYVCEGKAPFN
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complement(2130..2355)
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repeat_region complement(2816..3183)
/rpt_family="HAL1"
repeat_region complement(3290..3598)
/rpt_family="AluSg"
repeat_region complement(3611..3760)
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repeat_region complement(3766..4067)
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repeat_region complement(4803..5110)
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repeat_region 5266..5561
/rpt_family="AluSg"
repeat_region 5635..5932
/rpt_family="AluJo"
repeat_region 5984..6120
/rpt_family="AluJb"
repeat_region 6121..6423
/rpt_family="AluSx"
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repeat_region 6647..6913
/rpt_family="L1ME"
repeat_region 6936..7295
/rpt_family="MER33"
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repeat_region complement(10009..10303)
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STS 12180..12330
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strains include A/J, A/HeJ, 129/Sv, AKR/J, B10.D2-H2/OsNj, BALB/cByJ, BALB/cJ, C3H/HeJ, C57BL/6J, CAST/Ei, DBA/2J, MRL/MpJ, NZB/BinJ, NZW/Lac, SPRET/Ei."
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STS

ORIGIN

Query Match 87.0%; Score 17.4; DB 11; Length 600;
Best Local Similarity 94.7%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCA 19
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Db 160 AGGGCGTCTCCGAGTAGCA 178
|||||

RESULT 11

BV160504

LOCUS 600 bp DNA linear STS 15-MAY-2004
DEFINITION RPMWSE0038150 Roche Palo Alto Mus musculus STS genomic, sequence tagged site.

ACCESSION BV160504 GI:47263404

VERSION BV160504

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 600)

Usuka, J., Liao, G., Cheng, J., Nguyen, A., Bach, C., Puech, A.,

McPherson, J. D., Foerzler, D. and Peltz, G.

Mus musculus SNPs

Unpublished (2003)

CONTACT

Contact: Jonathan Usuka

Roche Palo Alto Genetics and Genomics Department

Roche Palo Alto

2431 Hillview Ave, Mailstop S3-1, Palo Alto, CA 94024, USA

Tel: 6508555807

Email: Jonathan.Usuka@roche.com

Primer A: No primer submitted with this STS

Primer B: No primer submitted with this STS.

FEATURES

source

1..600
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/map="17-7953-8459-CAAA01219574.1.1.20118"
/clone_lib="Roche Palo Alto"
/note="SNPs developed from assay sequences derived from 15 different strains of mice (as of October 1, 2003). Those strains include A/J, A/HeJ, 129/Sv, AKR/J, B10.D2-H2/OsNj, BALB/cByJ, BALB/cJ, C3H/HeJ, C57BL/6J, CAST/Ei, DBA/2J, MRL/MpJ, NZB/BinJ, NZW/Lac, SPRET/Ei."
<1..>600

STS

ORIGIN

Query Match 87.0%; Score 17.4; DB 11; Length 600;
Best Local Similarity 94.7%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCA 19
|||||

Db 160 AGGGCGTCTCCGAGTAGCA 178
|||||

RESULT 12

AB097568/c

LOCUS

AB097568 2095 bp mRNA linear ROD 28-APR-2004
DEFINITION Rattus norvegicus HAS1 mRNA for hyaluronan synthase 1, complete cds.

ACCESSION AB097568

VERSION AB097568.1 GI:26453348

KEYWORDS

SOURCE

ORGANISM

Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE

AUTHORS

Itano, N., Sawai, T., Atsumi, F., Miyaishi, O., Taniguchi, S.,

Kannagi, R., Hamauchi, M. and Kimata, K.

Selective expression and functional characteristics of three

Mammalian hyaluronan synthases in oncogenic malignant

transformation

J. Biol. Chem. 279 (18), 18679-18687 (2004)

14724275

REFERENCE

AUTHORS

Itano, N.

Direct Submission

Submitted (05-DEC-2002) Naoki Itano, Aichi Medical University,

Institute for Molecular Science of Medicine, Nagakute, Aichi, Aichi

480-1195, Japan [E-mail: itano@amugw.aichi-med-u.ac.jp,

Tel: 81-52-264-4811 (ex. 2095), Fax: 81-561-63-3532)

FEATURES

source

1..2095
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gene

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LADPYGLLAFLGLYCAFLSAHVAQSLFAYLEHRRVTVAARFAKGPJDAATARSVA

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PLDSWVFLSSLLRYWAVFNERACQSYFHCUSCISGPLGLYRNLLQOFLWAYNQKF

LGTCTGDDRLHTRMLSGYATKYTSRSCISPPSFLRWLSQOTRWSKSYFREW

LYNALWHRHAWMTYEAUVGLFPFFVAATVLRFLYAGRPWALLWLVLCVQGVALLAK

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ORIGIN

Query Match

Best Local Similarity 87.0%; Score 17.4; DB 10; Length 2095;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

1 AGGGCGTCTCTGAGTAGCA 19
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Db 1156 AGGGCGTCTCTGAGTAGCA 1138
|||||

RESULT 13

E13681/c

LOCUS

E13681 2102 bp DNA linear PAT 27-APR-1998

DEFINITION DNA encoding novel mouse hyaluronate synthetase.

ACCESSION

E13681

VERSION

E13681.1 GI:3252450

KEYWORDS

JP 1997224674-A/1.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 2102)

Itano, N. and Kimata, H.

FOLYPEPTIDE OF NEW HYALURONIC ACID-SYNTHETIC ENZYME AND DNA CODING

THE SAME

Patent: JP 1997224674-A 1 02-SEP-1997;

SCIENCE & TECH AGENCY

OS Mus musculus (mouse)

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PN JP 1997224674-A/1
PD 02-SEP-1997
PF 26-FEB-1996 JP 1996038336
PI ITANO NAOKI, KIMATA HIROHARU
PC C12N15/09, C07K14/47, C12N9/00//A61K48/00, C12N1/21, PC
(C12N9/00,
PC C12R1.91), (C12N9/00, C12R1.19), (C12N1/21, C12R1.19); CC
strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers
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/organism="Mus musculus"
/locus="E30971"
FT 5'UTR 1..48
FT CDS 49..1800
/feature="Novel mouse hyaluronate synthetase"
FT 3'UTR 1801..2102
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FEATURES
source
1..2102
Location/Qualifiers
/organism="Mus musculus"
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/db_xref="taxon:10090"
ORIGIN
Query Match 87.0%; Score 17.4; DB 6; Length 2102;
Best Local Similarity 94.7%; Pred. No. 8.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AGGGCGTCTCTCGAGTAGCA 19
|||||
Db 1162 AGGGCGTCTCCGAGTAGCA 1144

RESULT 14
LOCUS E28454/c 2102 bp DNA linear PAT 18-JUN-2001
DEFINITION Hyaluronate synthase promoter DNA.
ACCESSION E28454
VERSION E28454.1 GI:13018346
KEYWORDS JP 1999196875-A/2.
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Yoichi, Y., Naoki, I. and Koji, K.
TITLE Hyaluronate synthase promoter DNA
JOURNAL Patent: JP 1999196875-A 2 27-JUL-1999;
SEIKAGAKU KOGYO CO LTD
COMMENT OS Mus sp. (mouse)
PN JP 1999196875-A/2
PD 27-JUL-1999
PF 14-JAN-1998 JP 1998006191
PI YOICHI YAMADA, NAOKI ITANO, KOJI KIMATA
PC C12N15/09, C12N9/00, C12Q1/68// (C12N15/09, C12R1.91), C12N15/00,
(C12N15/00, C12R1.91)
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
FT CDS 49..1800.
Location/Qualifiers
1..2102
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ORIGIN
Query Match 87.0%; Score 17.4; DB 6; Length 2102;
Best Local Similarity 94.7%; Pred. No. 8.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AGGGCGTCTCTCGAGTAGCA 19
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Db 1162 AGGGCGTCTCCGAGTAGCA 1144

RESULT 15
LOCUS E30971/c 2102 bp DNA linear PAT 18-JUN-2001
DEFINITION Hyaluronate synthetase modified protein.
ACCESSION E30971
VERSION E30971.1 GI:13017286
KEYWORDS JP 2000004886-A/1.
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Naoki, I., Mamoru, Y. and Koji, K.
TITLE Hyaluronate synthetase modified protein
JOURNAL Patent: JP 2000004886-A 1 11-JAN-2000;
SEIKAGAKU KOGYO CO LTD
COMMENT OS Mus sp. (mouse)
PN JP 2000004886-A/1
PD 11-JAN-2000
PF 24-JUN-1998 JP 1998193788
PI NAOKI ITANO, MAMORU YOSHIDA, KOJI KIMATA
PC C12N15/09, C12N9/00, C12N15/00
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
FT CDS 49..1800.
Location/Qualifiers
1..2102
/organism="Mus sp."
/mol_type="genomic DNA"
/db_xref="taxon:10095"
ORIGIN
Query Match 87.0%; Score 17.4; DB 6; Length 2102;
Best Local Similarity 94.7%; Pred. No. 8.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AGGGCGTCTCTCGAGTAGCA 19
|||||
Db 1162 AGGGCGTCTCCGAGTAGCA 1144

RESULT 16
LOCUS E34326/c 2102 bp DNA linear PAT 31-JAN-2002
DEFINITION DNA for gene targeting hyaluronate synthase gene.
ACCESSION E34326
VERSION E34326.1 GI:18624311
KEYWORDS JP 2000116382-A/1.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Itano, N. and Kimata, K.
TITLE DNA for gene targeting hyaluronate synthase gene
JOURNAL Patent: JP 2000116382-A 1 25-APR-2000;
SEIKAGAKU KOGYO CO LTD
COMMENT OS Mus musculus (mouse)
PN JP 2000116382-A/1
PD 25-APR-2000
PF 13-OCT-1998 JP 1998291201
PI NAOKI ITANO, KOJI KIMATA
PC C12N15/09, C12N5/10, G01N33/50//C12N9/00, C12Q1/68, (C12N15/09, PC

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C12R1:91),
PC (C12N5/10, C12R1:91), C12N15/00, C12N5/00, (C12N15/00, C12R1:91),
PC (C12N5/00, C12R1:91)

CC FH Key Location/Qualifiers
FT CDS Location/Qualifiers

1..2102
49..1800.
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"

FEATURES

source

ORIGIN

Query Match 87.0%; Score 17.4; DB 6; Length 2102;
Best Local Similarity 94.7%; Pred. No. 8.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCA 19

Db 1162 AGGGCGTCTCCGAGTAGCA 1144

RESULT 17

MUSHAS/c

LOCUS MUSHAS 2102 bp mRNA linear ROD 06-FEB-1999
DEFINITION Mus musculus mRNA for hyaluronan synthase, complete cds.

ACCESSION D82964

VERSION D82964.1 GI:1339939

KEYWORDS hyaluronan synthase.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (sites)

Itano,N. and Kimata,K.

Expression cloning and molecular characterization of HAS protein, a
eukaryotic hyaluronan synthase

J. Biol. Chem. 271 (17), 9875-9878 (1996)

96215261

8626618

REFERENCE 2 (bases 1 to 2102)

PUBMED

Itano,N.

Unpublished

REFERENCE 3 (bases 1 to 2102)

Itano,N.

Direct Submission

Submitted (08-JAN-1996) Naoki Itano, Aichi Medical University,
Institute for Molecular Science of Medicine; Nagakute, Aichi-gun,
Aichi 480-11, Japan (Tel:052-264-4811(ex.2087), Fax:0561-63-3532)

Location/Qualifiers

1..2102

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/cell_line="FW3A H1"

/clone_lib="cDNA/pCDNA1"

49..1800

/codon_start=1

/product="hyaluronan synthase"

/protein_id="BAA11654.1"

/db_xref="GI:1339940"

/translation="MRQMPKPEAARCCSGLARRALTIIFALLILGLMTWAYAGVP
LASDRYGLLAFGLYGAFLSAHLAQSLPAYLEHRRVAAARSLAKGPLDAATARSVA
LTI SAYQEDPAYLRQCLVSARALLYPRALRLVMVDGNRFDLYMDFREVFADDE
PATYVWDGNTHQHPWEPAAGVAGVAREVEADPGRLAVALVTRRCVCVQARWG
GKREVMYAFKALGSDVYQVCDSDTRLDPALLLELVRLVDEDPVAGVGGDVRILN
PLDSWVSFLSLRYWFAFNVACQSYFHCVSCI SGPLGLYRNLLQOFLKAWYNQKF
LGTHCTFGDDRHLTNRMLSMGYATKTSRCSYSETPSSFLRWLSQOTRWSKSYFREW
LYNALWHRHHAWMYEA VVSGLFFEFVAATVIRLFPYAGRPHALLVLLVCVQVALAK
AAFAAWLRGRCVRLVSLYAPLYMCGLLPAKFLALVTMNSGWTSGRKKLAANYVPL
LPLALWALLLLGLLARSVAQEARADWSGFSRAAEAYHLAAGAGAYVAYVWMLTIYVW
GVRRLCRRRTGGYRVQV"

ORIGIN

Query Match 87.0%; Score 17.4; DB 9; Length 2109;
Best Local Similarity 94.7%; Pred. No. 8.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCA 19

Db 1149 AGGGTCTCTCTGAGTAGCA 1131

RESULT 19

AC108651_3

Query Match 87.0%; Score 17.4; DB 10; Length 2102;
Best Local Similarity 94.7%; Pred. No. 8.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCA 19

Db 1162 AGGGCGTCTCCGAGTAGCA 1144

RESULT 18

AY463695/c

LOCUS AY463695 2109 bp mRNA linear PRI 07-DEC-2003
DEFINITION Papio anubis hyaluronan synthase (HAS1) mRNA, complete cds.

ACCESSION AY463695

VERSION AY463695.1 GI:38607341

KEYWORDS

SOURCE

ORGANISM

Papio anubis (olive baboon)
Papio anubis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
Cercopitheciinae; Papio.

REFERENCE 1 (bases 1 to 2109)

AUTHORS Martinez-Duncker,I., Oriol,R. and Mollicone,R.

TITLE Evolution of the the hyaluronan, modulation c, chitin and cellulose

synthases: a superfamily of cell-wall associated carbohydrate

polymerizing enzymes

Unpublished

REFERENCE 2 (bases 1 to 2109)

AUTHORS Martinez-Duncker,I., Oriol,R. and Mollicone,R.

TITLE Direct Submission

JOURNAL Submitted (12-NOV-2003) Unite 504 Glycobiology Et Signalisation

Cellulaire, Inserm, 16 Avenue Paul Vaillant Couturier, Villejuif

94807, France

Location/Qualifiers

1..2109

/organism="Papio anubis"

/mol_type="mRNA"

/db_xref="taxon:9555"

1..2109

/gene="HAS1"

36..1787

/gene="HAS1"

/note="cell wall associated protein; produces hyaluronic

acid chains"

/codon_start=1

/product="hyaluronan synthase"

/protein_id="AAR25554.1"

/db_xref="GI:38607342"

/translation="NTQRTDPKTPAARRCCSGLARRVLTIFALLILGLMTWAYAGV
PLASDRYGLLAFGLYGAFLSAHLAQSLPAYLEHRRVAAARSLAKGPLDAATARSV
AUTI SAYQEDPAYLRQCLVSARALLYPRALRLVMVDGNRFDLYMDFREVFADDE
PATYVWDGNTHQHPWEPAAGVAGVAREVEADPGRLAVALVTRRCVCVQARWG
GKREVMYAFKALGSDVYQVCDSDTRLDPALLLELVRLVDEDPVAGVGGDVRILN
PLDSWVSFLSLRYWFAFNVACQSYFHCVSCI SGPLGLYRNLLQOFLKAWYNQKF
LGTHCTFGDDRHLTNRMLSMGYATKTSRCSYSETPSSFLRWLSQOTRWSKSYFREW
LYNALWHRHHAWMYEA VVSGLFFEFVAATVIRLFPYAGRPHALLVLLVCVQVALAK
AAFAAWLRGRCVRLVSLYAPLYMCGLLPAKFLALVTMNSGWTSGRKKLAANYVPL
LPLALWALLLLGLLARSVAQEARADWSGFSRAAEAYHLAAGAGAYVAYVWMLTIYVW
GVRRLCRRRTGGYRVQV"

ORIGIN

Query Match 87.0%; Score 17.4; DB 9; Length 2109;
Best Local Similarity 94.7%; Pred. No. 8.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCA 19

Db 1149 AGGGTCTCTCTGAGTAGCA 1131

WPCOMMENT

Sequence split into 4 fragments LOCUS AC108651 Accession AC108651
 Fragment Name Begin End
 AC108651_0 1 110000
 AC108651_1 100001 210000
 AC108651_2 200001 310000
 AC108651_3 300001 372955
 Continuation (4 of 4) of AC108651 Rattus norvegicus clone CH2

Query Match 87.0%; Score 17.4; DB 2; Length 72955;
 Best Local Similarity 94.7%; Pred. No. 3 4e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGCGTCTCTGAGTAGCA 19

Db 20251 AGGGCGTCTCTCAATAGCA 20269

RESULT 20

AC137058
 LOCUS AC137058 185623 bp DNA linear HTG 21-FEB-2003
 DEFINITION Papio anubis clone RP41-126M5, WORKING DRAFT SEQUENCE, 10 ordered pieces.

ACCESSION AC137058

VERSION AC137058.3 GI:28460766

KEYWORDS HTG; HTGS PHASE2; HTGS DRAFT.

SOURCE Papio anubis (olive baboon)

ORGANISM

Papio anubis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

Cercopithecinae; Papio.

1 (bases 1 to 185623)

AKter.N., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M.,
 Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
 Cariaga,K., Coleman,B., Engle,J., Granite,S., Guan,X., Gupta,J.,
 Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Idol,J.R., Karlins,E.,
 Laric,P., Lee-Lin,S.-Q., Legaapi,R., Maduro,Q.L., Maduro,V.B.,
 Maguilies,E.H., Masfello,C., Maskeri,B., McDowell,J.,
 Paquirigan,C., Pearson,R., Portnov,M.E., Prasad,A.,
 Reddi-Dugue,N., Schandler,K., Schueler,M.G., Sison,C.,
 Standtipop,S., Thomas,J.W., Thomas,P.J., Touchman,J.W., Vogt,J.L.,
 Wechterby,K.D., Wiggins,L., Young,A. and Green,E.D.
 NISC Comparative Sequencing Initiative

TITLE

JOURNAL
 REFERENCE 2 (bases 1 to 185623)

AUTHORS Green,E.D.

TITLE Direct Submission

JOURNAL Submitted (15-NOV-2002) NIH Intramural Sequencing Center, 8717

Government Circle, Gaithersburg, MD 20877, USA

REFERENCE 3 (bases 1 to 185623)

AUTHORS Green,E.D.

TITLE Direct Submission

JOURNAL Submitted (21-FEB-2003) NIH Intramural Sequencing Center, 8717

Government Circle, Gaithersburg, MD 20877, USA

On Feb 21, 2003 this sequence version replaced gi:27476124.

COMMENT

----- Genome Center
 Center: NIH Intramural Sequencing Center
 Center code: NISC
 Web site: <http://www.nisc.nih.gov>
 Contact: nisc_zoonhgri.nih.gov
 ----- Project Information
 Center project name: dtj
 Center clone name: 126M05

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8x average coverage in Q20 bases and has been reviewed to rule out

gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics

Sequencing vector: plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 183092 bases at least Q40
 Consensus quality: 183851 bases at least Q30
 Consensus quality: 184434 bases at least Q20
 Insert size: 160000; agarose-fp
 Insert size: 184723; sum-of-contigs
 Quality coverage: 14.13x in Q20 bases; agarose-fp
 Quality coverage: 12.24x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 10 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * provided by the submitter.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 1 9984: contig of 9984 bp in length

* 9985 10084: gap of unknown length

* 10085 49805: contig of 39721 bp in length

* 49806 49805: gap of unknown length

* 49906 68936: contig of 17031 bp in length

* 68937 67036: gap of unknown length

* 67037 83604: contig of 16568 bp in length

* 83605 83704: gap of unknown length

* 83705 108246: contig of 24542 bp in length

* 108247 108346: gap of unknown length

* 110221 110221: contig of 3675 bp in length

* 112121 112121: gap of unknown length

* 112122 134817: contig of 22696 bp in length

* 134818 134917: gap of unknown length

* 134918 147290: contig of 12373 bp in length

* 147291 147390: gap of unknown length

* 147391 185337: contig of 37947 bp in length

* 185338 185437: gap of unknown length

* 185438 185623: contig of 186 bp in length.

FEATURES

source

1. 185623
 /organism="Papio anubis"
 /mol_type="genomic DNA"
 /db_xref="taxon:9555"
 /clone="RP41-126M5"
 /clone_lib="RP41"

misc_feature

1. 15263
 /note="clone overlaps with GenBank Accession Number
 AC130273 clone RP41-30706 (center project name deu)"

misc_feature

1. .9984
 /note="assembly_fragment
 clone end:T7
 vector_side:left"

misc_feature

10085..49805
 /note="assembly_fragment"
 49906..68936
 /note="assembly_fragment"

misc_feature

67037..83604
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 83705..108246
 /note="assembly_fragment"

misc_feature

108347..112021
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 112122..134817
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misc_feature

134918..147290
 /note="assembly_fragment"
 147391..185337
 /note="assembly_fragment"

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGCGTCTCTGAGTAGCAG 20
|||||
Db 24219 GGGCTCTCTGAGTAGCAG 24237
|||||

RESULT 22

AL593846

LOCUS

DEFINITION Mouse DNA sequence from clone RP23-171H16 on chromosome 11,
complete sequence.

ACCESSION

AL593846

VERSION

AL593846.15 GI:20792584

KEYWORDS

HTG.

SOURCE

Mus musculus

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Tracey.A.

Direct Submission

Submitted (17-SEP-2003) Wellcome Trust Sanger Institute, Hinxton,

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On May 14, 2002 this sequence version replaced gi:19848059.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

The following abbreviations are used to associate primary accession

numbers given in the feature table with their source databases:

Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WormPEP; Information

on the WormPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep

Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: http://www.sanger.ac.uk

Contact: humquery@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all

regions were either double-stranded or sequenced with an alternate

chemistry or covered by high quality data (i.e. phred quality >

30); an attempt was made to resolve all sequencing problems, such

as compressions and repeats; all regions were covered by at least

one plasmid subclone or more than one M13 subclone; and the

assembly was confirmed by restriction digest, except on the rare

occasion of the clone being a YAC.

RP23-171H16 is from the RPCI-23 Mouse BAC Library

constructed by the group of Pieter de Jong.

For further details see http://www.chori.org/bacpac/home.htm

VECTOR: pBAC3.6

Sequence from the Mouse Genome Sequencing Consortium whole genome

shotgun may have been used to confirm this sequence. Sequence data

from the whole genome shotgun alone has only been used where it has

a phred quality of at least 30.

Location/Qualifiers

1. 213263

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

/chromosomes="11"

/clone_lib="RPCI-23"

/clone_id="RP23-171H16"

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/clone_lib="RPCI-23"

QY 1 AGGGCGTCTCTGAGTAGCA 19
|||||

Db 197418 AGGGCGTCTCTGAGTAGCA 197436
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RESULT 23

AC116203/c

LOCUS

DEFINITION

Rattus norvegicus clone CH230-148U11, *** SEQUENCING IN PROGRESS

***, 4 unordered pieces.

ACCESSION

AC116203

VERSION

GI:30579280

KEYWORDS

HTG; HTGS PHASE1; HTGS DRAFT; HTGS ENRICHED.

SOURCE

Rattus norvegicus (Norway rat)

ORGANISM

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

REFERENCE

1 (bases 1 to 257325)

AUTHORS

Muzny, D. Marie., Metzker, M. Lee., Abramson, S., Adams, C., Alder, J.,

Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,

Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,

Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,

Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,

Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,

Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,

Chacko, J., Chavez, D., Chen, R., Chen, Y., Chen, Z., Chu, J.,

Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,

Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,

Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,

Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,

Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,

Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,

Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,

Gebregorisis, E., Geer, K., Gill, R., Grady, M., Guerra, M., Guevara, W.,

Gharat, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K.,

Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,

Hernandez, R., Hines, S., Hlyuk, S., Hume, J., Idlebird, D., Jackson, A.,

Hollins, B., Howells, S., Hladun, S.L., Hodgson, A., Hogues, M.,

Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,

Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,

Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,

Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,

Lorensuwa, L., Loulseghe, H., Lozano, R.J., Lu, X., Ma, J.,

Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A.,

Mangum, B., Mapa, P., Martin, K., Martin, R., Martinez, E.,

Mawney, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,

Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,

Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,

Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,

Nwaekemele, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K.,

Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C.,

Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L.,

Puzo, M., Quirroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R.,

Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,

Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J.,

Sanders, W., Savery, G., Scherer, S., Scott, G., Shatman, S., Shen, H.,

Shetty, J., Shvartsbeyn, A., Sison, I., Sitter, C.D., Smajis, D.,

Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,

Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,

Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umani, K.,

Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J.,

Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, P.,

Williams, G., Willson, R., Wlezyk, R., Wooden, H., Worley, K.,

Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,

Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von

Niederhauser, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,

AC116203 257325 bp DNA linear HTG 13-MAY-2003

Rattus norvegicus clone CH230-148U11, *** SEQUENCING IN PROGRESS

***, 4 unordered pieces.

AC116203 4 GI:30579280

HTG; HTGS PHASE1; HTGS DRAFT; HTGS ENRICHED.

Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 257325)

Muzny, D. Marie., Metzker, M. Lee., Abramson, S., Adams, C., Alder, J.,

Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,

Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,

Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,

Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,

Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,

Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,

Chacko, J., Chavez, D., Chen, R., Chen, Y., Chen, Z., Chu, J.,

Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,

Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,

Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,

Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,

Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,

Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,

Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,

Gebregorisis, E., Geer, K., Gill, R., Grady, M., Guerra, M., Guevara, W.,

Gharat, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K.,

Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,

Hernandez, R., Hines, S., Hlyuk, S., Hume, J., Idlebird, D., Jackson, A.,

Hollins, B., Howells, S., Hladun, S.L., Hodgson, A., Hogues, M.,

Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,

Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,

Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,

Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,

Lorensuwa, L., Loulseghe, H., Lozano, R.J., Lu, X., Ma, J.,

Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A.,

Mangum, B., Mapa, P., Martin, K., Martin, R., Martinez, E.,

Mawney, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,

Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,

Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,

Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,

Nwaekemele, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K.,

Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C.,

Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L.,

Puzo, M., Quirroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R.,

Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,

Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J.,

Sanders, W., Savery, G., Scherer, S., Scott, G., Shatman, S., Shen, H.,

Shetty, J., Shvartsbeyn, A., Sison, I., Sitter, C.D., Smajis, D.,

Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,

Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,

Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umani, K.,

Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J.,

Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, P.,

Williams, G., Willson, R., Wlezyk, R., Wooden, H., Worley, K.,

Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,

Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von

Niederhauser, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,

Weinstock, G. and Gibbs, R.A.

Direct Submission

Unpublished

2 (bases 1 to 257325)

Worley, K.C.

Direct Submission

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL Submitted (26-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE 3 (bases 1 to 257325)

AUTHORS Rat Genome Sequencing Consortium.

TITLE Direct Submission

JOURNAL Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT On May 13, 2003 this sequence version replaced gi:23196079. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

----- Project Information
Center project name: GMMP
Center clone name: CH230-148J11

----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 222763 bases at least Q40
Consensus quality: 226733 bases at least Q30
Consensus quality: 228573 bases at least Q20
Estimated insert size: 243290; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 4050: contig of 4050 bp in length
* 4051 4150: gap of unknown length
* 4151 252607: contig of 248457 bp in length
* 252608 252707: gap of unknown length
* 252708 253739: contig of 1032 bp in length
* 253740 253839: gap of unknown length
* 253840 257325: contig of 3486 bp in length.

FEATURES Location/Qualifiers

source
1..257325
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-148J11"

misc_feature
1..1398
/note="wgs end_extension
clone_end:T7"

misc_feature
2650..3460
/note="clone boundary
clone_end:T7-
site:EcoRI
end_sequence:RWBA054TUB"

ORIGIN

Query Match 87.0%; Score 17.4; DB 2; Length 257325;
Best Local Similarity 94.7%; Pred. No. 2.5e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCA 19
|||||
Db 24113 AGGGCGTCTCTGAGTAGCA 24095
|||||

RESULT 24

AC079487 293184 bp DNA linear HTG 02-SEP-2000
Mus musculus clone RP23-182D19, WORKING DRAFT SEQUENCE, 35
unordered pieces.

AC079487
AC079487.1 GI:9964852
HTG; HTGS PHASE1; HTGS_DRAFT.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 293184)
DOE Joint Genome Institute.
Sequencing of Mouse
Unpublished
2 (bases 1 to 293184)
DOE Joint Genome Institute.
Direct Submission
Submitted (02-SEP-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

AUTHORS -----Genome Center
JOURNAL Center: Joint Genome Institute
TITLE Center Code: JGI
COMMENT Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 1806851
Center clone name: RPCI-23_182D19

Summary Statistics
Consensus quality: 271225 bases at least Q40
Consensus quality: 262829 bases at least Q30
Consensus quality: 285072 bases at least Q20
Estimated insert size: 242000; agarose-fp estimation
Estimated insert size: 289784; sum-of-contigs estimation
Quality coverage: 10.3 in Q20 bases; agarose-fp estimation
Quality coverage: 8.6 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 35 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1205: contig of 1205 bp in length
* 1206 1305: gap of unknown length
* 1306 2324: contig of 1019 bp in length
* 2325 2424: gap of unknown length
* 2425 3951: contig of 1527 bp in length
* 3952 4052: gap of unknown length
* 4053 5404: contig of 1253 bp in length
* 5405 5405: gap of unknown length
* 5405 6765: contig of 1361 bp in length
* 6766 6866: gap of unknown length
* 6866 9412: contig of 2547 bp in length
* 9413 9512: gap of unknown length
* 9513 11321: contig of 1809 bp in length
* 11322 11421: gap of unknown length
* 11422 13192: contig of 1771 bp in length
* 13193 13292: gap of unknown length
* 13293 14840: contig of 1548 bp in length
* 14841 16209: contig of 1269 bp in length
* 14941 16210: gap of unknown length

* 16310 17904: contig of 1595 bp in length
 * 17905 18004: gap of unknown length
 * 18005 19316: contig of 1312 bp in length
 * 19317 19416: gap of unknown length
 * 19417 21238: contig of 1822 bp in length
 * 21239 21338: gap of unknown length
 * 21339 25502: contig of 4184 bp in length
 * 25503 25602: gap of unknown length
 * 25603 27919: contig of 2317 bp in length
 * 27920 28019: gap of unknown length
 * 28020 31424: contig of 3405 bp in length
 * 31425 31524: gap of unknown length
 * 31525 34478: contig of 2954 bp in length
 * 34479 34578: gap of unknown length
 * 34580 39184: contig of 4606 bp in length
 * 39185 39284: gap of unknown length
 * 39285 43661: contig of 4377 bp in length
 * 43662 43761: gap of unknown length
 * 43762 49966: contig of 6205 bp in length
 * 49967 50667: gap of unknown length
 * 50668 56743: contig of 6677 bp in length
 * 56744 56843: gap of unknown length
 * 56844 64029: contig of 7186 bp in length
 * 64030 64129: gap of unknown length
 * 64130 71006: contig of 6877 bp in length
 * 71007 71106: gap of unknown length
 * 71107 79434: contig of 8328 bp in length
 * 79435 79534: gap of unknown length
 * 79535 92429: contig of 12895 bp in length
 * 92430 92529: gap of unknown length
 * 92530 111247: contig of 18718 bp in length
 * 111248 111347: gap of unknown length
 * 111348 122768: contig of 11421 bp in length
 * 122769 122868: gap of unknown length
 * 122869 141721: contig of 18853 bp in length
 * 141722 141821: gap of unknown length
 * 141822 156874: contig of 15053 bp in length
 * 156875 156974: gap of unknown length
 * 156975 176989: contig of 20015 bp in length
 * 176990 177089: gap of unknown length
 * 177090 197198: contig of 20109 bp in length
 * 197199 197298: gap of unknown length
 * 197299 215257: contig of 17959 bp in length
 * 215258 215357: gap of unknown length
 * 215358 230320: contig of 14963 bp in length
 * 230321 230420: gap of unknown length
 * 230421 256851: contig of 26431 bp in length
 * 256852 256951: gap of unknown length
 * 256952 293184: contig of 36233 bp in length.

FEATURES
 source
 1..293184
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 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /clone="RP23-182D19"
 /clone_lib="RPCI mouse BAC library 23"

ORIGIN
 Query Match 87.0%; Score 17.4; DB 2; Length 293184;
 Best Local Similarity 94.7%; Pred. No. 2.4e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCGAGTAGCA 19
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 DB 277530 AGGGCGTCTCGAGTAGCA 277548

RESULT 25
 AX898222
 LOCUS AX898222 278 bp DNA linear PAT 18-DEC-2003
 DEFINITION Sequence 14085 from Patent EP1033401.
 ACCESSION AX898222
 VERSION AX898222.1 GI:40053135

KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 1 Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
 Expressed sequence tags and encoded human proteins
 JOURNAL Patent: EP 1033401-A 14085 06-SEP-2000;
 Genset (FR)

FEATURES
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 Location/Qualifiers
 1..278
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
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ORIGIN
 Query Match 84.0%; Score 16.8; DB 6; Length 278;
 Best Local Similarity 90.0%; Pred. No. 2.7e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCGAGTAGCAG 20
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 DB 113 AGGGCATCTCTGAGTTGCAG 132

RESULT 26
 BD033755
 LOCUS BD033755 278 bp DNA linear PAT 27-AUG-2002
 DEFINITION Sequence tag and encoded human protein.
 ACCESSION BD033755
 VERSION BD033755.1 GI:22575497
 KEYWORDS JP 2001269182-A/10001.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 1 (bases 1 to 278)
 AUTHORS Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
 TITLE Sequence tag and encoded human protein
 JOURNAL Patent: JP 2001269182-A 10001 02-OCT-2001;
 GENSET

COMMENT
 OS Homo sapiens (human)
 PN JP 2001269182-A/10001
 PD 02-OCT-2001
 PR 24-FEB-2000 JP 2000118773
 PR 26-FEB-1999 US 60/122487
 PI JEAN BAPTISTE DUMAS MILNE EDWARDS, BIMERIC DUCLAIR, JEAN YVES
 PI JORDAN
 PC C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21, PC
 C12N5/10.
 PC C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC
 G06F15/40
 CC

FEATURES
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 Location/Qualifiers
 1..278
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

ORIGIN
 Query Match 84.0%; Score 16.8; DB 6; Length 278;
 Best Local Similarity 90.0%; Pred. No. 2.7e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCGAGTAGCAG 20
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 DB 113 AGGGCATCTCTGAGTTGCAG 132

RESULT 27
 AX886427

LOCUS AX886427 313 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 2290 from Patent EP1033401.
ACCESSION AX886427
VERSION AX886427.1 GI:40043577
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
AUTHORS Expressed sequence tags and encoded human proteins
TITLE Patent: EP 1033401-A 2290 06-SEP-2000;
JOURNAL Genset (FR)
FEATURES
source
1..313
/organism="Homo sapiens"
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103..>312
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QRLPLCLLVLTITKGRPLVCFINEP"
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Query Match 84.0%; Score 16.8; DB 6; Length 313;
Best Local Similarity 90.0%; Pred. No. 2.6e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AGGGCGTCTCTGAGTAGCAG 20
||||| ||||||| |||||
Db 113 AGGGCATCTCTGAGTTGCAG 132
RESULT 28
LOCUS BD026037 313 bp DNA linear PAT 27-AUG-2002
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD026037
VERSION BD026037.1 GI:22567260
KEYWORDS JP 2001269182-A/2283.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 313)
REFERENCE Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
AUTHORS Sequence tag and encoded human protein
TITLE Patent: JP 2001269182-A 2283 02-OCT-2001;
JOURNAL GENSET
COMMENT OS Homo sapiens (human)
PN JP 2001269182-A/2283
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PI 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES
PI JORDAN
PI C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10,
PC C12P21/02,C12P21/08,C13Q1/68//G06F17/30,C12N15/00,C12N5/00, PC
G06F15/40
CC OS
FH Key Location/Qualifiers
FT CDS 103..312.
FEATURES
source
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 84.0%; Score 16.8; DB 6; Length 313;
Best Local Similarity 90.0%; Pred. No. 2.6e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AGGGCGTCTCTGAGTAGCAG 20
||||| ||||||| |||||
Db 113 AGGGCATCTCTGAGTTGCAG 132
RESULT 29
LOCUS AF367431 465 bp mRNA linear PRI 24-MAY-2001
DEFINITION Homo sapiens clone 0484e082 placental protein 13-like mRNA, partial
cds.
ACCESSION AF367431
VERSION AF367431.1 GI:14194180
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 465)
REFERENCE Yang,Q.-S., Xie,Y. and Mao,Y.M.
AUTHORS Cloning and expression pattern study of a novel human galectin
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 465)
AUTHORS Yang,Q.-S., Xie,Y. and Mao,Y.M.
TITLE Direct Submission
JOURNAL Submitted (04-APR-2001) Research Institute of Genetics, School of
Life Science, 220 Handan Rd., Shanghai 200433, China
FEATURES
source
1..465
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="19"
/map="19q13.1"
/clone="0484e082"
/tissue_type="brain"
/dev_stage="18 week fetus"
224..>465
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/product="placental protein 13-like"
/protein_id="AAK56285.1"
/db_xref="GI:14194181"
/translation="MSSLFVPVYTLPSLVPVSGVILTGPIILTFVKDPLEVNFYTG
DEDSDIATQFRLHFGHPAIMNSCVFGIWRYEKCY"
ORIGIN
Query Match 84.0%; Score 16.8; DB 9; Length 465;
Best Local Similarity 90.0%; Pred. No. 2.3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AGGGCGTCTCTGAGTAGCAG 20
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Db 127 AGGGCATCTCTGAGTTGCAG 146
RESULT 30
LOCUS AF367432 529 bp mRNA linear PRI 24-MAY-2001
DEFINITION Homo sapiens clone 0484e083 placental protein 13-like mRNA, partial
cds.
ACCESSION AF367432
VERSION AF367432.1 GI:14194182
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 529)
REFERENCE Yang,Q.-S., Xie,Y. and Mao,Y.M.
AUTHORS

TITLE Cloning and expression pattern study of a novel human galectin
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 529)
AUTHORS Yang,Q.-S., Xie,Y. and Mao,Y.M.
TITLE Direct Submission
JOURNAL Submitted (04-APR-2001) Research Institute of Genetics, School of Life Science, 220 Handan Rd., Shanghai 200433, China

FEATURES
source
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="19"
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/clone="0484e083"
/tissue_type="brain"
/dev_stage="18 week fetus"
224..>529
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/product="placental protein 13-like"
/protein_id="AAK56286.1"
/db_xref="GI:14194183"
/translation="MSSLPLVPVPTLPSLPVSGSVIITGTPILTFVKDPQLEVNFYTM"
DEDSDIAQFRLHFGHPAIMNSCVFIWRYBEKCYLLPFEDGKPFELCIYVRHKYKV
"

ORIGIN
Query Match 84.0%; Score 16.8; DB 9; Length 529;
Best Local Similarity 90.0%; Pred.No.2.3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CDS
1 AGGGCGTCTCTGAGTAGCAG 20
|||||
127 AGGGCATCTCTGAGTTGCAG 146

RESULT 31
AF367430 536 bp mRNA linear PRI 24-MAY-2001
LOCUS Homo sapiens clone 0484e081 placental protein 13-like mRNA, partial cds
DEFINITION
ACCESSION AF367430
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Yang,Q.-S., Xie,Y. and Mao,Y.M.
TITLE Cloning and expression pattern study of a novel human galectin
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 536)
AUTHORS Yang,Q.-S., Xie,Y. and Mao,Y.M.
TITLE Direct Submission
JOURNAL Submitted (04-APR-2001) Research Institute of Genetics, School of Life Science, 220 Handan Rd., Shanghai 200433, China

FEATURES
source
Location/Qualifiers
1..536
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="19"
/map="19q13.1"
/clone="0484e081"
/tissue_type="brain"
/dev_stage="18 week fetus"
224..>536
/codon_start=1
/product="placental protein 13-like"
/protein_id="AAK56284.1"
/db_xref="GI:14194179"
/translation="MSSLPLVPVPTLPSLPVSGSVIITGTPILTFVKDPQLEVNFYTM"

CDS
1 AGGGCGTCTCTGAGTAGCAG 20
|||||
127 AGGGCATCTCTGAGTTGCAG 146

RESULT 32
AF367430 555 bp DNA linear STS 31-MAY-2003
LOCUS S212P60157FH3.TO CZECHII/Ei Mus musculus STS genomic, sequence tagged site.
DEFINITION
ACCESSION BV037702
VERSION BV037702.1 GI:31121597
KEYWORDS STS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 555)
AUTHORS Wade,C.M., Kulbokas,E.J. III, Kirby,A.W., Zody,M.C., Mullikin,J.C., Lander,E.S., Lindblad-Toh,K. and Daly,M.J.
TITLE The mosaic structure of variation in the laboratory mouse genome
JOURNAL Nature 420 (6915), 574-578 (2002)
MEDLINE 22354684
PUBMED 12466852

COMMENT
Contact: Kerstin Lindblad-Toh
Whitehead Institute for Biomedical Research, Center for Genome Research
320 Charles Street, Cambridge, MA 02141, USA
Tel: 6172521477
Fax: 6172580903
Email: kersli@genome.wi.mit.edu
Primer A: None
Primer B: None
STS size: 555
Protocol:
WGS-discovery: Paired-end low-coverage whole genome shotgun reads were generated from 129S1/SvImJ, C3H/HeJ, and BALB/cByJ. The WGS reads were placed uniquely on the MGS CV3 C57BL/6J assembly and SNP detection was carried out by SSAHA-SNP. 225,000 reads were annotated as STSs and 81,000 SNPs were annotated with alleles from C57BL/6J and the strain from which the particular read came. The validation rate for these SNPs was estimated at approximately 98%.

FEATURES
source
Location/Qualifiers
1..555
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="CZECHII/Ei"
/db_xref="taxon:10090"
/map="9 12-492 120522219-120522688"
/clone_lib="CZECHII/Ei"
<1..>555

STS
ORIGIN
Query Match 84.0%; Score 16.8; DB 11; Length 555;
Best Local Similarity 90.0%; Pred.No.2.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY
1 AGGGCGTCTCTGAGTAGCAG 20
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127 AGGGCATCTCTGAGTTGCAG 146

RESULT 33
AG367430 386 AGGGTGTCTCTGAGTAGCAG 405
|||||

TITLE Cloning and expression pattern study of a novel human galectin
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 529)
AUTHORS Yang,Q.-S., Xie,Y. and Mao,Y.M.
TITLE Direct Submission
JOURNAL Submitted (04-APR-2001) Research Institute of Genetics, School of Life Science, 220 Handan Rd., Shanghai 200433, China

FEATURES
source
Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="19"
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/clone="0484e083"
/tissue_type="brain"
/dev_stage="18 week fetus"
224..>529
/codon_start=1
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/protein_id="AAK56286.1"
/db_xref="GI:14194183"
/translation="MSSLPLVPVPTLPSLPVSGSVIITGTPILTFVKDPQLEVNFYTM"
DEDSDIAQFRLHFGHPAIMNSCVFIWRYBEKCYLLPFEDGKPFELCIYVRHKYKV
"

ORIGIN
Query Match 84.0%; Score 16.8; DB 9; Length 529;
Best Local Similarity 90.0%; Pred.No.2.3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CDS
1 AGGGCGTCTCTGAGTAGCAG 20
|||||
127 AGGGCATCTCTGAGTTGCAG 146

RESULT 31
AF367430 536 bp mRNA linear PRI 24-MAY-2001
LOCUS Homo sapiens clone 0484e081 placental protein 13-like mRNA, partial cds
DEFINITION
ACCESSION AF367430
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Yang,Q.-S., Xie,Y. and Mao,Y.M.
TITLE Cloning and expression pattern study of a novel human galectin
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 536)
AUTHORS Yang,Q.-S., Xie,Y. and Mao,Y.M.
TITLE Direct Submission
JOURNAL Submitted (04-APR-2001) Research Institute of Genetics, School of Life Science, 220 Handan Rd., Shanghai 200433, China

FEATURES
source
Location/Qualifiers
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/dev_stage="18 week fetus"
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/db_xref="GI:14194179"
/translation="MSSLPLVPVPTLPSLPVSGSVIITGTPILTFVKDPQLEVNFYTM"

CDS
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127 AGGGCATCTCTGAGTTGCAG 146

RESULT 32
AF367430 555 bp DNA linear STS 31-MAY-2003
LOCUS S212P60157FH3.TO CZECHII/Ei Mus musculus STS genomic, sequence tagged site.
DEFINITION
ACCESSION BV037702
VERSION BV037702.1 GI:31121597
KEYWORDS STS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 555)
AUTHORS Wade,C.M., Kulbokas,E.J. III, Kirby,A.W., Zody,M.C., Mullikin,J.C., Lander,E.S., Lindblad-Toh,K. and Daly,M.J.
TITLE The mosaic structure of variation in the laboratory mouse genome
JOURNAL Nature 420 (6915), 574-578 (2002)
MEDLINE 22354684
PUBMED 12466852

COMMENT
Contact: Kerstin Lindblad-Toh
Whitehead Institute for Biomedical Research, Center for Genome Research
320 Charles Street, Cambridge, MA 02141, USA
Tel: 6172521477
Fax: 6172580903
Email: kersli@genome.wi.mit.edu
Primer A: None
Primer B: None
STS size: 555
Protocol:
WGS-discovery: Paired-end low-coverage whole genome shotgun reads were generated from 129S1/SvImJ, C3H/HeJ, and BALB/cByJ. The WGS reads were placed uniquely on the MGS CV3 C57BL/6J assembly and SNP detection was carried out by SSAHA-SNP. 225,000 reads were annotated as STSs and 81,000 SNPs were annotated with alleles from C57BL/6J and the strain from which the particular read came. The validation rate for these SNPs was estimated at approximately 98%.

FEATURES
source
Location/Qualifiers
1..555
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="CZECHII/Ei"
/db_xref="taxon:10090"
/map="9 12-492 120522219-120522688"
/clone_lib="CZECHII/Ei"
<1..>555

STS
ORIGIN
Query Match 84.0%; Score 16.8; DB 11; Length 555;
Best Local Similarity 90.0%; Pred.No.2.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY
1 AGGGCGTCTCTGAGTAGCAG 20
|||||
127 AGGGCATCTCTGAGTTGCAG 146

RESULT 33
AG367430 386 AGGGTGTCTCTGAGTAGCAG 405
|||||

AF267852 774 bp mRNA linear PRI 11-JUN-2002
 LOCUS Homo sapiens placental protein 13-like protein mRNA, complete cds.
 DEFINITION
 ACCESSION AF267852
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 774)
 AUTHORS Yang Q.S., Ying, K., Yuan, H.L., Chen, J.Z., Meng, X.F., Wang, Z., Xie, Y. and Mao, Y.M.
 TITLE Cloning and expression of a novel human galectin cDNA, predominantly expressed in placenta(1)
 JOURNAL Biochim. Biophys. Acta 1574 (3), 407-411 (2002)
 MEDLINE 21992454
 PUBMED 11997112
 REFERENCE 2 (bases 1 to 774)
 AUTHORS Mao, Y.M., Xie, Y., Yuan, H.L., Yang, Q.S., Wu, H., Xia, P. and Ying, K.
 TITLE Direct Submission
 JOURNAL Submitted (15-MAY-2000) Institute of Genetics, Fudan University, 220 Handan Rd., Shanghai 200433, China
 FEATURES
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 /organism="Homo sapiens"
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 DSDSDIAFQRLHFHGPALMNSCVGIWYERKCYLPEDGKPELCLIVYRHKYKV
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 CDS
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 ORIGIN
 Query Match 84.0%; Score 16.8; DB 9; Length 774;
 Best Local Similarity 90.0%; Pred. No. 2.1e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AGGGCGTCTCTGAGTAGCAG 20
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 Db 127 AGGGCATCTCTGAGTTGCAG 146
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 RESULT 34
 BV063966 795 bp DNA linear STS 31-MAY-2003
 LOCUS S212P6739FB3.T0 CZECHII/Bi Mus musculus STS genomic, sequence tagged site.
 DEFINITION
 ACCESSION BV063966
 VERSION BV063966.1 GI:31179761
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 795)
 AUTHORS Wade, C.M., Kulbokas, E.J. III, Kirby, A.W., Zody, M.C., Mullikin, J.C., Lander, E.S., Lindblad-Toh, K. and Daly, M.J.
 TITLE The mosaic structure of variation in the laboratory mouse genome
 JOURNAL Nature 420 (6915), 574-578 (2002)
 MEDLINE 22354684
 PUBMED 12466852
 COMMENT
 Contact: Kerstin Lindblad-Toh
 Whitehead Institute for Biomedical Research, Center for Genome Research

320 Charles Street, Cambridge, MA 02141, USA
 Tel: 6172521477
 Fax: 6172580903
 Email: kersl@genome.wi.mit.edu
 Primer A: None
 Primer B: None
 STS size: 795
 Protocol:
 WGS-discovery: Paired-end low-coverage whole genome shotgun reads were generated from 12981/SvIm7, C3H/HeJ, and BALB/cByJ. The WGS reads were placed uniquely on the MGSCV3 C57BL/6J assembly and SNP detection was carried out by SSAHA-SNP. 225,000 reads were annotated
 as STSs and 81,000 SNPs were annotated with alleles from C57BL/6J and the strain from which the particular read came. The validation rate for these SNPs was estimated at approximately 98%.
 FEATURES
 source
 1. 795
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="CZECHII/Sl"
 /db_xref="taxon:10090"
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 /clone_lib="CZECHII/Sl"
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 ORIGIN
 Query Match 84.0%; Score 16.8; DB 11; Length 795;
 Best Local Similarity 90.0%; Pred. No. 2e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AGGGCGTCTCTGAGTAGCAG 20
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 Db 283 AGGGCTTCTCTGAGGAGCAG 302
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 RESULT 35
 AK056640/c 3111 bp mRNA linear PRI 30-JAN-2004
 LOCUS Homo sapiens cDNA FLJ32078 fis, clone OCBF1000192.
 DEFINITION
 ACCESSION AK056640
 VERSION
 KEYWORDS oligo capping; fis (full insert sequence).
 SOURCE Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS
 Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Sugawara, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hirakawa, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yoda, M., Hootuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T.,

Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yanashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S. Complete sequencing and characterization of 21,243 full-length human cDNAs Nat. Genet. 36 (1), 40-45 (2004)

14702039
2
Oshima, A., Takahashi-Fujii, A., Tanase, T., Imose, N., Takeuchi, K., Arita, M., Musashino, K., Yuuki, H., Hara, H., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Ota, T., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahori, K., Masuho, Y., Nagai, K. and Isogai, T.
NEDO human cDNA sequencing project
Unpublished
3 (bases 1 to 3111)
Isogai, T., Otsuki, T. and Sugiyama, T.
Direct Submission
Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and HRI.

TITLE Location/Qualifiers
JOURNAL 1..3111
PUBMED /organism="Homo sapiens"
REFERENCE /mol_type="mRNA"
AUTHORS /db_xref="taxon:9606"
JOURNAL /clone="OCBPF1000192"
/tissue_type="brain"
/clone_lib="OCBPF1"
/dev_stage="fetus"
/note="cloning vector: pME18SFL3"

COMMENT

FEATURES
source
1..3111
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="OCBPF1000192"
/tissue_type="brain"
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/dev_stage="fetus"
/note="cloning vector: pME18SFL3"

ORIGIN
Query Match 84.0%; Score 16.8; DB 9; Length 3111;
Best Local Similarity 90.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AGGGGGCTCTCTGAGTAGCAG 20
|||||
Db 380 AGGGAGTCTCTGAGAGCAG 361
|||||

RESULT 36
AC006133
LOCUS 43859 bp DNA linear PRI 05-DEC-1998
DEFINITION Homo sapiens chromosome 19, cosmid R30692, complete sequence.
ACCESSION AC006133
VERSION AC006133.1 GI:3970929
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 43859)
Lamerdin, J.E., McCreedy, P.M., Skowronski, E., Visswanathan, V., Burkhardt-Schultz, K.J., Gordon, L., Dias, J., Ramirez, M., Stiilwagen, S., Phan, H., Velasco, N., Do, L., Regala, W., Terry, A., Barnes, J., Danganan, L., Erler, A., Christensen, M., Georgescu, A., Avila, J., Liu, S., Attis, C., Andreise, T., Trankheim, M., Amico-Keller, G., Coefield, J., Duarte, S., Lucas, S., Bruce, R., Thomas, P., Quan, G., Kronmiller, B., Arellano, A., Sanders, C., Ow, D.,

Nolan, M., Trong, S., Kobayashi, A., Olsen, A.S. and Carrano, A.V. Sequence analysis of a 2.3 Mb region in 19q13.1 containing the RYR gene Unpublished
2 (bases 1 to 43859)
Lamerdin, J.E.
Direct Submission
Submitted (05-DEC-1998) Joint Genome Institute, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA

TITLE Location/Qualifiers
JOURNAL 1..43859
PUBMED /organism="Homo sapiens"
REFERENCE /mol_type="genomic DNA"
AUTHORS /db_xref="taxon:9606"
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/note="Cosmid library constructed at LLNL from flow-sorted chromosomes from hybrid 5HL2-B, which carries chromosome 19 as its only human chromosome."

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complement(3392..3483)
/note="predicted exon, program: grail2exons_human_1.3, frame: 1, quality: excellent, score: 92.000"
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4846..5140
repeat_region /rpt_family="AluJb"
5141..5936
repeat_region /rpt_family="L1PA14"
6328..6465
repeat_region /rpt_family="AluJo/FRAM"
complement(6508..6702)
repeat_region /rpt_family="AluY"
6703..7517
repeat_region /rpt_family="L1PA13"
complement(8575..8639)
repeat_region /rpt_family="(CA)n"
9297..9594
repeat_region /rpt_family="AluJo"
complement(9947..10157)
repeat_region /rpt_family="MIR"
complement(11543..11844)
repeat_region /rpt_family="AluSx"
complement(13142..13250)
misc_feature /note="predicted exon, program: grail2exons_human_1.3, frame: 0, quality: excellent, score: 96.000"
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/note="predicted exon, program: grail2exons_human_1.3, frame: 1, quality: excellent, score: 75.000"
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complement(16389..16538)
repeat_region /rpt_family="L1MG"
complement(16533..17661)
repeat_region /rpt_family="L1PB1"
complement(17692..23827)
repeat_region /rpt_family="L1PA2"
23871..24384
repeat_region /rpt_family="L1PA7"
complement(24392..24418)
repeat_region /rpt_family="(TA)n"
24716..24994
repeat_region /rpt_family="AluJo"

repeat_region	25011. .25061 /rpt_family="POLY_A" complement(25163. .25206)	AC100349 Mus musculus clone RP23-127117, DNA linear HTG 22-NOV-2001
repeat_region	/rpt_family="LINE2" complement(25483. .25514)	AC100349.1 GI:17047715 HTG; HTGS PHASE0.
repeat_region	/rpt_family="(CA)n" complement(25571. .25674)	Mus musculus (house mouse)
repeat_region	/rpt_family="AT_rich" 25678. .26197	Mus musculus
repeat_region	/rpt_family="MERS7_internal" 26198. .29570	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
repeat_region	/rpt_family="L1PA2" complement(29571. .29596)	1 (bases 1 to 45136) Birren,B., Linton,L., Nusbaum,C. and Lander,E.
repeat_region	/rpt_family="(CA)n" 30686. .30872	Unpublished
repeat_region	/rpt_family="MIR" complement(31135. .31436)	2 (bases 1 to 45136) Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
repeat_region	/rpt_family="AluJo" 32539. .32720	Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., ChoepeI,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heatford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Lakocque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G., McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., O'Liver,J., Peterson,K., Phunkhang,P., Pierre,N., Risse,C., Rogov,P., Raymond,C., Retta,R., Rieback,M., Riley,R., Rie,C., Pollara,V., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seanan,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
misc_feature	/note="predicted exon, program: grail2exons_human_1.3, frame: 0, quality: good, score: 54.000" complement(35136. .35240)	Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
misc_feature	/note="predicted exon, program: grail2exons_human_1.3, frame: 0, quality: excellent, score: 93.000" 35489. .35615	All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
repeat_region	/rpt_family="LINE2" complement(35769. .35823)	----- Genome Center
repeat_region	/rpt_family="(TAA)n" complement(35825. .36529)	Center: Whitehead Institute/ MIT Center for Genome Research
repeat_region	/rpt_family="L1PA2" 36528. .36970	Center code: WIBR
misc_feature	/rpt_family="L1PA2" complement(38018. .38228)	Web site: http://www-seq.wi.mit.edu
repeat_region	/note="1, quality: excellent, score: 95.000" complement(39070. .39349)	Contact: sequence submissions@genome.wi.mit.edu
repeat_region	/rpt_family="AluJb" 39358. .39500	----- Project Information
repeat_region	/rpt_family="MIR" complement(39643. .39922)	Center project name: L15145
repeat_region	/rpt_family="LMC/D" 39928. .39997	Center clone name: 127_I_17
repeat_region	/rpt_family="(GAA)n" complement(40156. .40227)	-----
repeat_region	/rpt_family="AluJo" 40228. .40527	* NOTE: This record contains 44 individual
repeat_region	/rpt_family="AluSx" complement(40528. .40738)	* sequencing reads that have not been assembled into
misc_feature	/rpt_family="AluJo" complement(42119. .42194)	* contigs. Runs of N are used to separate the reads
repeat_region	/note="predicted exon, program: grail2exons_human_1.3, frame: 0, quality: excellent, score: 81.000" 42395. .42445	* and the order in which they appear is completely
repeat_region	/rpt_family="L1PB1" complement(42453. .42587)	* arbitrary. Low-pass sequence sampling is useful for
repeat_region	/rpt_family="HERVL" complement(43512. .43591)	* identifying clones that may be gene-rich and allows
repeat_region	/rpt_family="AT_rich" 43753. .43799	* overlap relationships among clones to be deduced.
	/rpt_family="LINE2"	* However, it should not be assumed that this clone
		* will be sequenced to completion. In the event that
		* the record is updated, the accession number will
		* be preserved.
		* 1
		* 934 933: contig of 933 bp in length
		* 1034 1033: gap of 100 bp
		* 1960 1960: contig of 927 bp in length
		* 1961 2060: gap of 100 bp
		* 2061 2979: contig of 919 bp in length
		* 2980 3079: gap of 100 bp
		* 3080 3977: contig of 898 bp in length
		* 3978 4077: gap of 100 bp
		* 4078 5018: contig of 941 bp in length
		* 5019 5118: gap of 100 bp
		* 5119 6088: contig of 970 bp in length
		*
ORIGIN		
Query Match	84.0%; Score 16.8; DB 9; Length 43859;	
Best Local Similarity	90.0%; Pred. No. 7.5e+02;	
Matches 18; Conservative	0; Mismatches 2; Indels 0; Gaps 0;	
Qy	1 AGGGCGCTCTGAGTAGCAG 20	
Db	8167 AGGGCATCTCTGAGTTGCAG 8186	
RESULT 37		
, AC100349/c		

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* 6089 6188: gap of 100 bp
* 7044: contig of 856 bp in length
* 7045 7144: gap of 100 bp
* 8032: contig of 888 bp in length
* 8033 8132: gap of 100 bp
* 8133 9027: contig of 895 bp in length
* 9028 9127: gap of 100 bp
* 9128 10040: contig of 913 bp in length
* 10041 10140: gap of 100 bp
* 10141 11108: contig of 968 bp in length
* 11109 11208: gap of 100 bp
* 11209 12041: contig of 833 bp in length
* 12042 12141: gap of 100 bp
* 12142 13050: contig of 909 bp in length
* 13051 13150: gap of 100 bp
* 13151 14095: contig of 945 bp in length
* 14096 14195: gap of 100 bp
* 14196 15050: contig of 855 bp in length
* 15051 15150: gap of 100 bp
* 15151 16097: contig of 947 bp in length
* 16098 16197: gap of 100 bp
* 16198 17167: contig of 970 bp in length
* 17168 17267: gap of 100 bp
* 17268 18207: contig of 940 bp in length
* 18208 18307: gap of 100 bp
* 18308 19191: contig of 884 bp in length
* 19192 19291: gap of 100 bp
* 19292 20292: contig of 1001 bp in length
* 20293 20392: gap of 100 bp
* 20393 21236: contig of 844 bp in length
* 21237 21336: gap of 100 bp
* 21337 22266: contig of 930 bp in length
* 22267 22366: gap of 100 bp
* 22367 23345: contig of 973 bp in length
* 23346 24365: contig of 920 bp in length
* 24366 25116: contig of 951 bp in length
* 25117 25516: gap of 100 bp
* 25518 26511: contig of 995 bp in length
* 26512 27513: contig of 902 bp in length
* 27514 28575: contig of 962 bp in length
* 28576 29572: contig of 897 bp in length
* 29573 29672: gap of 100 bp
* 29673 30706: contig of 934 bp in length
* 30707 31662: contig of 956 bp in length
* 31663 32704: contig of 942 bp in length
* 32705 32804: gap of 100 bp
* 32805 33651: contig of 847 bp in length
* 33652 33751: gap of 100 bp
* 33752 34685: contig of 934 bp in length
* 34686 34785: gap of 100 bp
* 34786 35685: contig of 900 bp in length
* 35686 35785: gap of 100 bp
* 35786 36754: contig of 969 bp in length
* 36755 37764: contig of 910 bp in length
* 37765 38004: gap of 100 bp
* 38005 38904: gap of 100 bp
* 38906 39865: contig of 961 bp in length
* 39866 39965: gap of 100 bp
* 39966 40921: contig of 956 bp in length
* 40922 41021: gap of 100 bp
* 41022 41934: contig of 913 bp in length
* 41935 42034: gap of 100 bp
* 42035 43049: contig of 1015 bp in length
* 43050 43149: gap of 100 bp

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* 43150 44107: contig of 958 bp in length
* 44108 44207: gap of 100 bp
* 44208 45136: contig of 929 bp in length.
FEATURES
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            /mol_type="genomic DNA"
            /db_xref="taxon:10090"
            /clone="RP23-127117"
            /clone_lib="RPCI-23 Female Mouse BAC"
ORIGIN
Query Match      84.0%; Score 16.8; DB 2; Length 45136;
Best Local Similarity 90.0%; Pred. No. 7.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AGGGCGTCTCTGAGTAGCAG 20
    |||||
DB 23870 AGGGCGACTCGAGTAGCAG 23851
    |||||
RESULT 38
AC016271/c
LOCUS
DEFINITION Homo sapiens clone RP11-19F12, LOW-PASS SEQUENCE SAMPLING.
ACCESSION AC016271
VERSION AC016271.2 GI:9123891
KEYWORDS HTG; HTGS_PHASE0.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 80065)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens, clone RP11-19F12
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 80065)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boquelavkiy,L., Boukhalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., DeArelano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczky,J., Lien,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tefaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wymann,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (24-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced gi:6467063.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L3728
Center clone name: 19_F_12
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* NOTE: This record contains 82 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows

```

* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1	903: contig of 903 bp in length	
* 904	1003: gap of 100 bp	33212
* 1004	1895: contig of 892 bp in length	34120
* 1896	1995: gap of 100 bp	34220
* 2890	2890: contig of 895 bp in length	35104
* 2891	2990: gap of 100 bp	35204
* 2991	3816: contig of 826 bp in length	36064
* 3817	3916: gap of 100 bp	36164
* 3917	4776: contig of 860 bp in length	37033
* 4777	4876: gap of 100 bp	37133
* 4877	5746: contig of 870 bp in length	37034
* 5747	5846: gap of 100 bp	38021
* 5947	6741: contig of 895 bp in length	38121
* 6742	6841: gap of 100 bp	38122
* 6842	7705: contig of 864 bp in length	39019
* 7706	7805: gap of 100 bp	39119
* 7806	8688: contig of 883 bp in length	40035
* 8689	8789: gap of 100 bp	40134
* 8789	9660: contig of 872 bp in length	41047
* 9661	9760: gap of 100 bp	41147
* 9761	10661: contig of 901 bp in length	41148
* 10662	10761: gap of 100 bp	42068
* 10762	11625: contig of 864 bp in length	42069
* 11626	11725: gap of 100 bp	42169
* 11726	12619: contig of 894 bp in length	43149
* 12620	12719: gap of 100 bp	44028
* 12720	13621: contig of 902 bp in length	44128
* 13622	13721: gap of 100 bp	44990
* 13722	14582: contig of 861 bp in length	45090
* 14583	14682: gap of 100 bp	45957
* 14683	15537: contig of 855 bp in length	46056
* 15538	15637: gap of 100 bp	46940
* 15638	16517: contig of 880 bp in length	47041
* 16518	16617: gap of 100 bp	47940
* 16618	17504: contig of 887 bp in length	48040
* 17505	17604: gap of 100 bp	48831
* 17605	18479: contig of 875 bp in length	49794
* 18480	18579: gap of 100 bp	50800
* 18580	19458: contig of 879 bp in length	51769
* 19459	19558: gap of 100 bp	51869
* 19559	20428: contig of 870 bp in length	52724
* 20429	20528: gap of 100 bp	52824
* 20529	21424: contig of 896 bp in length	53687
* 21425	21524: gap of 100 bp	53787
* 21525	22423: contig of 899 bp in length	54672
* 22424	22523: gap of 100 bp	54772
* 22524	23367: contig of 844 bp in length	55657
* 23368	23467: gap of 100 bp	55757
* 23468	24369: contig of 902 bp in length	56645
* 24370	24469: gap of 100 bp	56745
* 24470	25324: contig of 855 bp in length	57638
* 25325	25424: gap of 100 bp	57738
* 25425	26267: contig of 843 bp in length	58617
* 26268	26367: gap of 100 bp	58717
* 26368	27235: contig of 868 bp in length	59556
* 27236	27335: gap of 100 bp	59656
* 27336	28210: contig of 875 bp in length	60556
* 28211	28310: gap of 100 bp	61341
* 28311	29200: contig of 890 bp in length	61641
* 29201	29300: gap of 100 bp	61642
* 29301	30174: contig of 874 bp in length	62548
* 30175	30274: gap of 100 bp	62648
* 30275	31162: contig of 888 bp in length	63492
* 31163	31262: gap of 100 bp	63592
* 31263	32105: contig of 843 bp in length	64445
* 32106	32205: gap of 100 bp	64545
* 32206	33111: contig of 906 bp in length	65421
* 33112	33211: gap of 100 bp	65521

34119: contig of 908 bp in length
34219: gap of 100 bp
35103: contig of 884 bp in length
35203: gap of 100 bp
36064: contig of 861 bp in length
36164: gap of 100 bp
37033: contig of 869 bp in length
37133: gap of 100 bp
38021: contig of 888 bp in length
38121: gap of 100 bp
38122: contig of 897 bp in length
39019: gap of 100 bp
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40035: gap of 100 bp
40134: contig of 913 bp in length
41047: contig of 921 bp in length
41147: gap of 100 bp
41148: contig of 921 bp in length
42068: gap of 100 bp
42069: contig of 880 bp in length
43149: gap of 100 bp
44028: contig of 879 bp in length
44128: gap of 100 bp
44990: contig of 862 bp in length
45090: gap of 100 bp
45957: contig of 867 bp in length
46056: gap of 100 bp
46940: contig of 884 bp in length
47041: gap of 100 bp
47940: contig of 899 bp in length
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48831: contig of 791 bp in length
49794: contig of 863 bp in length
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51869: gap of 100 bp
52724: contig of 855 bp in length
52824: gap of 100 bp
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62548: contig of 906 bp in length
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64545: gap of 100 bp
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65521: gap of 100 bp
65521: contig of 876 bp in length
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67377: gap of 100 bp
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68377: gap of 100 bp
68378: contig of 883 bp in length
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* 69361 69460: gap of 100 bp
 * 69461 70336: contig of 876 bp in length
 * 70337 70436: gap of 100 bp
 * 70437 71288: contig of 852 bp in length

Query Match 84.0%; Score 16.8; DB 2; Length 80065;
 Best Local Similarity 90.0%; Pred. No. 6.e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
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 Db 77537 AGGGAGTCTCTGAGAGCAG 77518

RESULT 39

CR382131_11/c

WPCOMMENT

Sequence split into 43 fragments LOCUS CR382131 Accession CR382131

Fragment Name	Begin	End
CR382131_00	1	110000
CR382131_01	100001	210000
CR382131_02	200001	310000
CR382131_03	300001	410000
CR382131_04	400001	510000
CR382131_05	500001	610000
CR382131_06	600001	710000
CR382131_07	700001	810000
CR382131_08	800001	910000
CR382131_09	900001	1010000
CR382131_10	1000001	1110000
CR382131_11	1100001	1210000
CR382131_12	1200001	1310000
CR382131_13	1300001	1410000
CR382131_14	1400001	1510000
CR382131_15	1500001	1610000
CR382131_16	1600001	1710000
CR382131_17	1700001	1810000
CR382131_18	1800001	1910000
CR382131_19	1900001	2010000
CR382131_20	2000001	2110000
CR382131_21	2100001	2210000
CR382131_22	2200001	2310000
CR382131_23	2300001	2410000
CR382131_24	2400001	2510000
CR382131_25	2500001	2610000
CR382131_26	2600001	2710000
CR382131_27	2700001	2810000
CR382131_28	2800001	2910000
CR382131_29	2900001	3010000
CR382131_30	3000001	3110000
CR382131_31	3100001	3210000
CR382131_32	3200001	3310000
CR382131_33	3300001	3410000
CR382131_34	3400001	3510000
CR382131_35	3500001	3610000
CR382131_36	3600001	3710000
CR382131_37	3700001	3810000
CR382131_38	3800001	3910000
CR382131_39	3900001	4010000
CR382131_40	4000001	4110000
CR382131_41	4100001	4210000
CR382131_42	4200001	4224103

Continuation (12 of 43) of CR382131 from base 1100001 (CR382131 Yarrowia lipolytica chr6)

Query Match 84.0%; Score 16.8; DB 8; Length 110000;
 Best Local Similarity 90.0%; Pred. No. 6.e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
 ||||| ||||| ||||| |||||
 Db 99278 ACGGGCTCTCTGAGTAGCG 99259

RESULT 40

AC106708

LOCUS

DEFINITION

BAC Library

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AC106708 127109 bp DNA linear PRI 12-JUN-2002
 Homo sapiens 3 BAC RP11-392A22 (Roswell Park Cancer Institute Human
 BAC Library) complete sequence.

AC106708

AC106708.7 GI:21392433

HTG.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 127109)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-ouman, F.R., Allen, C.,
 Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayale, M., Banks, T.,
 Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D.,
 Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,
 Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
 Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
 Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
 Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
 Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
 Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
 Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
 Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
 Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
 Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
 Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
 Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., He, X.,
 Hernandez, J., Hernandez, O., Hodgson, A., Hogue, M., Holloway, C.,
 Hollins, B., Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J.,
 Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,
 Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
 Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C.,
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 Louis, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R.,
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 Mei, G., Metzker, M., Miner, Z., Mitchell, T., Mohabbat, K.,
 Moore, S., Morgan, M., Moorish, T., Morris, S., Moser, M., Neal, D.,
 Nelson, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N.,
 Nickerson, E., Nwokenkwo, S., Ogihara, W., Okunolu, G., Oragunye, N.,
 Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L.,
 Pickens, R., Primus, E., Pu, L., Quiles, M., Ren, Y., Rives, M.,
 Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savary, G., Scherer, S.,
 Scott, G., Shen, H., Shoohtari, N., Sison, I., Sodergren, E.,
 Sonaiki, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A.,
 Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C.,
 Taylor, T., Telford, B., Thomas, N., Thomas, S., Umami, K., Vasquez, L.,
 Vera, V., Villalón, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S.,
 Warren, R., Washington, C., Watlington, S., Williams, G.,
 Williamson, A., Wleczek, R., Wooden, S., Worley, K., Wu, C., Wu, Y.,
 Wu, Y.F., Zhou, J., Zorrilla, S., Naylor, S.L., Weinstein, G. and
 Gibbs, R.

TITLE

Direct Submission

Unpublished

2 (bases 1 to 127109)

Worley, K.C.

TITLE

Direct Submission

Submitted (12-JAN-2002) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 127109)

Worley, K.C.

TITLE

Direct Submission

Submitted (07-JUN-2002) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

4 (bases 1 to 127109)

Worley, K.C.

TITLE

Direct Submission

Submitted (12-JUN-2002) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

COMMENT

Baylor Plaza, Houston, TX 77030, USA
On Jun 12, 2002 this sequence version replaced gi:21328473.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email
gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL:
<http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

FEATURES

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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="3"
/clone="RP11-392A22"

misc_feature

1. .2000
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/function="clone overlap"

repeat_region

1. .469
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repeat_region

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repeat_region

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repeat_region

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repeat_region

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repeat_region

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repeat_region

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repeat_region

complement(9816. .10114)
/rpt_family="AluSx"

repeat_region

complement(10355. .10396)
/rpt_family="MIR"

repeat_region

11331. .11520

repeat_region /rpt_family="AluSg/x"
12355. .12458
/rpt_family="MLT1L"
repeat_region 14405. .14425
/rpt_family="GC_rich"
repeat_region 14791. .14821
/rpt_family="GC_rich"
repeat_region complement(15997. .16301)
/rpt_family="AluY"
repeat_region complement(16453. .16742)
/rpt_family="AluJo"
repeat_region 16748. .16780
/rpt_family="AT_rich"
repeat_region 17344. .17430
/rpt_family="AT_rich"
repeat_region complement(17616. .17685)
/rpt_family="L2"
repeat_region 18061. .18192
/rpt_family="MER91A"
repeat_region 20378. .20402
/rpt_family="AT_rich"
repeat_region 20569. .20827
/rpt_family="CTCG)n"
STS 20714. .20836
/standard_name="89729"
repeat_region complement(22797. .22844)
/rpt_family="MIR"
repeat_region complement(22837. .22970)
/rpt_family="L2"
repeat_region 24520. .24611
/rpt_family="MIR"
repeat_region 24766. .24812
/rpt_family="GGA)n"
repeat_region complement(25517. .25721)
/rpt_family="LIME"
repeat_region complement(26143. .26253)
/rpt_family="MER94"
repeat_region 26505. .26539
/rpt_family="CA)n"
repeat_region 27978. .28054
/rpt_family="MLT1L"
repeat_region 28289. .28656
/rpt_family="MLT1A2"
repeat_region 29260. .29427
/rpt_family="MER5A"
repeat_region complement(29760. .29892)
/rpt_family="MIR"
repeat_region complement(30077. .30368)
/rpt_family="AluSx"
repeat_region 30445. .30783
/rpt_family="L2"
repeat_region 30784. .31147
/rpt_family="THE1B"
repeat_region 31148. .31596
/rpt_family="L2"
repeat_region 31621. .32138

Query Match 84.0%; Score 16.8; DB 9; Length 127109;

Best Local Similarity 90.0%; Pred. No. 5.8e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20

DB 53952 AGGGCTTCTCTGAGGAGCAG 53971

RESULT 41

AL731701/c

LOCUS

DEFINITION

Mouse DNA

sequence.

ACCESSION

AL731701

VERSION

128198 bp DNA linear

sequence from clone RP23-140L6 on chromosome X, complete

AL731701

GI:22449772

KEYWORDS
SOURCE
ORGANISM
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 128198)
REFERENCE
AUTHORS
 Heath, P.
TITLE
JOURNAL
 Direct Submission
 Submitted (20-AUG-2002) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
 On Aug 22, 2002 this sequence version replaced gi:21912692.
COMMENT
 ----- Genome Center
 Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: <http://www.sanger.ac.uk>
 Contact: humquery@sanger.ac.uk

 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >=
 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. The following
 abbreviations are used to associate primary accession numbers given
 in the feature table with their source databases: Em: EMBL; Sw:
 SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP
 database can be found at
<http://www.sanger.ac.uk/projects/C.elegans/wormpep> RP23-140L6 is
 from the RPCI-23 Mouse PAC Library
 constructed by the group of Pieter de Jong.
 For further details see <http://www.chori.edu/bacpac/home.htm>
 VECTOR: pBACE3.6
FEATURES
 source
 1..128198
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /chromosome="X"
 /clone="RP23-140L6"
 /clone_lib="RPCI-23"
ORIGIN
 Query Match 84.0%; Score 16.8; DB 10; Length 128198;
 Best Local Similarity 90.0%; Pred. No. 5.8e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AGGGCGTCTCTGAGTAGCAG 20
 ||||| ||||| ||||| ||||| |||||
 Db 10533 AGGGCGACTCGGAGTAGCAG 10514
 RESULT 42
 AC026671
LOCUS
DEFINITION
 Homo sapiens 3 BAC RP11-91M9 (Roswell Park Cancer Institute Human
 BAC Library) complete sequence.
ACCESSION
 AC026671
VERSION
 AC026671.18 GI:18921226
KEYWORDS
 HTG.
SOURCE
 Homo sapiens (human)
ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 141674)
REFERENCE
AUTHORS
 Muzny, D.M., Adams, C., Ali-Osman, B., Ali-Osman, F.R., Allen, C.,

Alsbrooks, S.L., Amaraturunge, H.C., Are, J.R., Ayele, M., Banks, T.,
 Barbara, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D.,
 Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,
 Buhay, P., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
 Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
 Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
 Cleveland, C.D., Cox, C., Coyle, M.D., Bathorne, S.R., David, R.,
 Davilan, M.L., Davis, C., Davy-Carrroll, L., Dederich, D.A.,
 Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, K.H.,
 Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
 Earhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
 Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
 Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
 Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
 Harris, K., Harris, K., Hart, M., Havlak, P., Hawes, A., He, X.,
 Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C.,
 Hollins, B., Honsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J.,
 Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,
 Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
 Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C.,
 Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,
 Louie, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R.,
 Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A.,
 Martinez, E., Massey, E., Mawhinney, E., McLeod, M.P., Meador, M.,
 Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K.,
 Moore, S., Morgan, M., Moorish, T., Morris, S., Moser, M., Neal, D.,
 Nelson, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N.,
 Nickerson, E., Nwokwenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N.,
 Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, J., Peters, L.,
 Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, J., Rivers, M.,
 Rojas, A., Rojebokan, I., Roife, M., Ruiz, S., Savery, G., Scherer, S.,
 Scott, G., Shen, H., Shoohtari, N., Sisson, I., Sodergren, E.,
 Sonaik, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A.,
 Tabor, P., Tanerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C.,
 Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L.,
 Vera, V., Villalobos, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S.,
 Warren, R., Washington, C., Watlington, S., Williams, G.,
 Williamson, A., Wleczek, R., Wooden, S., Worley, K., Wu, C., Wu, Y.,
 Wu, Y.F., Zhou, J., Zorrilla, S., Naylor, S.L., Weinstein, G. and
 Gibbs, R.
 Direct Submission
 Unpublished
 2 (bases 1 to 141674)
 Worley, K.C.
 Direct Submission
 Submitted (23-MAR-2000) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 141674)
 Worley, K.C.
 Direct Submission
 Submitted (26-FEB-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 4 (bases 1 to 141674)
 Worley, K.C.
 Direct Submission
 Submitted (31-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Feb 26, 2002 this sequence version replaced gi:18644817.
 INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email
 gc-help@bcm.tmc.edu
CLONE LENGTH: This sequence does not necessarily represent the
 entire insert of this clone. Overlapping regions of clones are only
 sequenced and submitted once, so the sequence for the remainder of
 the insert may be found in the record for the adjacent clones.
 Overlapping clones are noted at the beginning and end of the
 Features listing.
ANNOTATION OF FEATURES:
 STSs are identified using ePCR (Genome Res. 7:541-550) searches

of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT.

FEATURES

source

Location/Qualifiers
1. .141674
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="3"
/clone="RP11-91M9"

misc_feature

1. .2005
/notes="overlaps bases 13201. .15205 of clone AC079847"

repeat_region

function="clone overlap"
complement(236. .616)
/rpt_family="MER69"
complement(720. .1140)
/rpt_family="MER69"
complement(1287. .1371)
/rpt_family="MIR"
1401. .1472
/rpt_family="TATG)n"
complement(2954. .3069)
/rpt_family="L2"
complement(3249. .3420)
/rpt_family="MERSA"
complement(3451. .3538)
/rpt_family="MERSB"
complement(3879. .3957)
/rpt_family="L2"
4314. .4633
/rpt_family="AluSg1"
complement(6384. .6597)
/rpt_family="L2"
6598. .6895
/rpt_family="AluSg1"
complement(6896. .7058)
/rpt_family="L2"
complement(7086. .7397)
/rpt_family="L2"
7996. .8087
/rpt_family="MIR"
8281. .8367
/rpt_family="MIR"
9088. .9173
/rpt_family="L2"
complement(9712. .10010)
/rpt_family="AluSg"
10311. .10333
/rpt_family="AT_rich"
12072. .12272

repeat_region
13526. .13817
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13996. .14127
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complement(14715. .14974)
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14978. .15029
/rpt_family="CATATA)n"
16007. .16178
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16464. .16969
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complement(18618. .18796)
/rpt_family="LIME3A"
complement(18888. .19460)
/rpt_family="LIM4"
19515. .19621
/rpt_family="MER91C"
complement(19634. .19782)
/rpt_family="HAL1"
complement(19860. .20182)
/rpt_family="LIM3c"
20236. .20265
/rpt_family="AT_rich"
complement(20938. .21235)
/rpt_family="AluY"
21862. .21886
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23464. .23516
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23517. .23545
/rpt_family="AT_rich"
23785. .24137
/rpt_family="THE1A"
25710. .26061
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26742. .26784
/rpt_family="(TG)n"
complement(26819. .27044)
/rpt_family="L2"
27553. .27608

Query Match 84.0%; Score 16.8; DB 9; Length 141674;
Best Local Similarity 90.0%; Pred.No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGCGGCTCTCTCAGTAGCAG 20
Db 11754 AGCGATTCTCTGAGTAGCAG 11773

RESULT 43

AL627204
LOCUS Mouse DNA sequence from clone RP23-118E21 on chromosome 4, complete sequence.
DEFINITION AL627204
ACCESSION AL627204
VERSION AL627204.7 GI:21953005
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 142447)
AUTHORS Iad.H.
TITLE Direct Submission
JOURNAL Submitted (19-JUL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
COMMENT On Jul 24, 2002 this sequence version replaced gi:21615588. ----- Genome Center
Center: Wellcome Trust Sanger Institute

Center code: SC
 Web site: <http://www.sanger.ac.uk>
 Contact: humquery@sanger.ac.uk

 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Swi., SWISSPROT; Tr., TrEMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-118E21 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: pBAC3.6.

FEATURES
 source
 1..142447
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /chromosomes="4"
 /clone="RP23-118E21"
 /clone_lib="RPCI-23"

ORIGIN
 Query Match 84.0%; Score 16.8; DB 10; Length 142447;
 Best Local Similarity 90.0%; Pred. No. 5.6e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
 |||||
 Db 125628 AGGGCGTCTCTGAGGAGGAG 125647

RESULT 44
 AC142379/c

LOCUS
 DEFINITION Rattus norvegicus clone CH230-428C22, *** SEQUENCING IN PROGRESS
 ,, 52 unordered pieces.

ACCESSION
 AC142379.1 GI:29336148
 VERSION HTG; HTGS_PHASE1.
 KEYWORDS Rattus norvegicus (Norway rat)
 SOURCE Rattus norvegicus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE
 1 (bases 1 to 144791)
 Muzny,D.Marie., Metzker,M.Lee., Abramson,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Caldwell,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,K., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Kocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,

Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jollivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowls,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorenshewa,L., Loulsegged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangun,P., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhney,S., McLeod,M., McNeill,T., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaakeleneh,O., Okwuonu,G., Olanrunsgoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkuch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,P., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingley,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villagana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstein,G. and Gibbs,R.A.

Direct Submission
 Unpublished
 2 (bases 1 to 144791)
 Worley,K.C.

Direct Submission
 Submitted (28-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu

----- Project Information
 Center project name: KEJR
 Center clone name: CH230-428C22

----- Summary Statistics
 Sequencing vector: Plasmid;
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 109373 bases at least Q40
 Consensus quality: 118449 bases at least Q30
 Consensus quality: 124461 bases at least Q20
 Estimated insert size: 115919; sum-of-contigs estimation
 Quality coverage: 2x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 52 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 1120: contig of 1120 bp in length
 * 1121 1220: gap of unknown length
 * 1221 2245: contig of 1025 bp in length

* 2246 2345: gap of unknown length
* 2346 3765: contig of 1420 bp in length
* 3766 3865: gap of unknown length
* 3866 4902: contig of 1037 bp in length
* 4903 5002: gap of unknown length
* 5003 6331: contig of 1329 bp in length
* 6332 6431: gap of unknown length
* 6432 7644: contig of 1213 bp in length
* 7645 7744: gap of unknown length
* 7745 8790: contig of 1046 bp in length
* 8791 8890: gap of unknown length
* 8891 10769: contig of 1879 bp in length
* 10770 10869: gap of unknown length
* 10870 12171: contig of 1302 bp in length
* 12172 12271: gap of unknown length
* 12273 13631: contig of 1360 bp in length
* 13632 13731: gap of unknown length
* 13733 15082: contig of 1351 bp in length
* 15083 15182: gap of unknown length
* 15183 16360: contig of 1178 bp in length
* 16361 16460: gap of unknown length
* 16462 17642: contig of 1182 bp in length
* 17643 17742: gap of unknown length
* 17743 19814: contig of 2072 bp in length
* 19815 19914: gap of unknown length
* 19916 21109: contig of 1195 bp in length
* 21110 21209: gap of unknown length
* 21210 23322: contig of 2113 bp in length
* 23323 23422: gap of unknown length
* 23423 24487: contig of 1065 bp in length
* 24488 24587: gap of unknown length
* 24588 26099: contig of 1512 bp in length
* 26100 26199: gap of unknown length
* 26200 27227: contig of 1028 bp in length
* 27228 27327: gap of unknown length
* 27328 28359: contig of 1032 bp in length
* 28360 28459: gap of unknown length
* 28460 30141: contig of 1682 bp in length
* 30142 30241: gap of unknown length
* 30242 32324: contig of 2083 bp in length
* 32325 32424: gap of unknown length
* 32425 34042: contig of 1618 bp in length
* 34043 34142: gap of unknown length
* 34143 35445: contig of 1303 bp in length
* 35446 35545: gap of unknown length
* 35546 37447: contig of 1902 bp in length
* 37448 37547: gap of unknown length
* 37548 38795: contig of 1248 bp in length
* 38796 38895: gap of unknown length
* 38896 40985: contig of 2090 bp in length
* 40986 41085: gap of unknown length
* 41086 44415: contig of 3330 bp in length
* 44416 44515: gap of unknown length
* 44516 46750: contig of 2235 bp in length
* 46751 46850: gap of unknown length
* 46851 49596: contig of 2746 bp in length
* 49597 49696: gap of unknown length
* 49697 53101: contig of 3405 bp in length
* 53102 53201: gap of unknown length
* 53202 55283: contig of 2082 bp in length
* 55284 55383: gap of unknown length
* 55384 57687: contig of 2304 bp in length
* 57688 57787: gap of unknown length
* 57788 60536: contig of 2749 bp in length
* 60537 60636: gap of unknown length
* 60637 63422: contig of 2786 bp in length
* 63423 63522: gap of unknown length
* 63523 66737: contig of 3215 bp in length
* 66738 66837: gap of unknown length
* 66838 69284: contig of 2447 bp in length
* 69285 69384: gap of unknown length
* 69385 72049: contig of 2665 bp in length
* 72050 72149: gap of unknown length

* 72150 74727: contig of 2578 bp in length
* 74728 74827: gap of unknown length
* 74828 78115: contig of 3288 bp in length
* 78116 78215: gap of unknown length
* 78216 83524: contig of 5309 bp in length
* 83525 83624: gap of unknown length
* 83625 88051: contig of 4427 bp in length
* 88052 88151: gap of unknown length
* 88152 89634: contig of 1483 bp in length
* 89635 89734: gap of unknown length
* 89735 95449: contig of 5715 bp in length
* 95450 95549: gap of unknown length
* 95550 99104: contig of 3555 bp in length
* 99105 99204: gap of unknown length
* 99205 104067: contig of 4863 bp in length
* 104068 104167: gap of unknown length
* 104168 109882: contig of 5715 bp in length
* 109883 109982: gap of unknown length
* 109983 114844: contig of 4862 bp in length
* 114845 114944: gap of unknown length
* 114945 120216: contig of 5272 bp in length
* 120217 120316: gap of unknown length
* 120317 127452: contig of 7135 bp in length
* 127452 127552: gap of unknown length
* 127552 135387: contig of 7836 bp in length
* 135388 135487: gap of unknown length
* 135488 144791: contig of 9304 bp in length.

FEATURES Location/Qualifiers

Query Match 84.0%; Score 16.8; DB 2; Length 144791;
Best Local Similarity 90.0%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGGCTCTCTAGTAGCAG 20
||||| ||||| ||||| |||||
Db 94987 AGGGCTCTCTGTAGCAG 94968

RESULT 45

AC073808 149727 bp DNA linear HTG 18-JUL-2000
LOCUS Mus musculus clone RP23-53L19, WORKING DRAFT SEQUENCE, 23 ordered
DEFINITION pieces.

ACCESSION AC073808
VERSION AC073808.2 GI:9256809
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 149727)

AUTHORS DOE Joint Genome Institute.

TITLE Sequencing of Mouse

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 149727)

AUTHORS DOE Joint Genome Institute.

TITLE Direct Submission

JOURNAL

COMMENT Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 18, 2000 this sequence version replaced gi:8810425.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information

Center Project Name: 1757507

Center clone name: RPCI-23_53L19

Summary Statistics

Consensus quality: 138531 bases at least Q40

Consensus quality: 145586 bases at least Q30

Consensus quality: 146846 bases at least Q20

Estimated insert size: 167000; agarose-fp estimation
 Estimated insert size: 148677; sum-of-ctnigs estimation
 Quality coverage: 6.17 in Q20 bases; agarose-fp estimation
 Quality coverage: 6.93 in Q20 bases; sum-of-ctnigs estimation.
 * NOTE: This is a 'working draft' sequence. It currently

* consists of 23 ctnigs. Gaps between the ctnigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * provided by the submittor.

* This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * by the accession number will be preserved.

* 1 24435: contig of 24435 bp in length

* 24436 24535: gap of unknown length

* 24536 25237: contig of 702 bp in length

* 25238 25337: gap of unknown length

* 25338 27179: contig of 1842 bp in length

* 27180 27279: gap of unknown length

* 27280 37150: contig of 9871 bp in length

* 37151 37250: gap of unknown length

* 37251 43105: contig of 5855 bp in length

* 43106 43205: gap of unknown length

* 43206 44356: contig of 1051 bp in length

* 44357 44356: gap of unknown length

* 44357 57901: contig of 13545 bp in length

* 57902 58001: gap of unknown length

* 58002 71982: contig of 13981 bp in length

* 71983 72082: gap of unknown length

* 72083 79704: contig of 7622 bp in length

* 79705 79804: gap of unknown length

* 79805 84158: gap of unknown length

* 84159 86603: contig of 2445 bp in length

* 86604 92822: contig of 6119 bp in length

* 92823 105052: gap of unknown length

* 105053 105152: gap of unknown length

* 105153 106141: contig of 989 bp in length

* 106142 106241: gap of unknown length

* 106242 110743: contig of 4502 bp in length

* 110744 110843: gap of unknown length

* 110844 112176: contig of 1333 bp in length

* 112177 112276: gap of unknown length

* 112277 128768: contig of 16492 bp in length

* 128769 128868: gap of unknown length

* 128869 131960: contig of 3092 bp in length

* 131961 132060: gap of unknown length

* 132061 137483: contig of 5423 bp in length

* 137484 137583: gap of unknown length

* 137584 142994: contig of 5411 bp in length

* 142995 143094: gap of unknown length

* 143095 145122: contig of 2028 bp in length

* 145123 145222: gap of unknown length

* 145223 148984: contig of 3762 bp in length

* 148985 149084: gap of unknown length

* 149085 149727: contig of 643 bp in length.

* 149085 Location/Qualifiers

1. .149727

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

/clone="RP23-531u9"

/clone_lib="RPC1 mouse BAC library 23"

84.0%; Score 16.8; DB 2; Length 149727;

Best Local Similarity 90.0%; Pred.No. 5.5e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

ORIGIN

1 AGGGCGTCTCTGAGTAGCAG 20

||||| ||||||| |||||

Query Match 84.0%; Score 16.8; DB 2; Length 149727;

Best Local Similarity 90.0%; Pred.No. 5.5e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

ORIGIN

1 AGGGCGTCTCTGAGTAGCAG 20

||||| ||||||| |||||

Query Match 84.0%; Score 16.8; DB 2; Length 149727;

Best Local Similarity 90.0%; Pred.No. 5.5e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

ORIGIN

1 AGGGCGTCTCTGAGTAGCAG 20

||||| ||||||| |||||

Db 68753 AGGGAGTCTCTGAGAGCAG 68772

RESULT 46

AC104782/c

LOCUS

AC104782

DEFINITION

AC104782

ACCESSION

AC104782.5

VERSION

GI:19551164

KEYWORDS

HTG.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 150010)

Toward a complete human genome sequence

Genome Res. 8 (11), 1097-1108 (1998)

99063792

9847074

2 (bases 1 to 150010)

Waligorski, J., Kozlowski, A., Spalding, L. and Bielicki, L.

The sequence of Homo sapiens BAC clone RP11-30G7

Unpublished (2001)

3 (bases 1 to 150010)

Waterston, R.H.

Direct Submission

Submitted (21-DEC-2001) Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

4 (bases 1 to 150010)

Waterston, R.H.

Direct Submission

Submitted (15-FEB-2002) Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

5 (bases 1 to 150010)

Waterston, R.H.

Direct Submission

Submitted (20-MAR-2002) Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

6 (bases 1 to 150010)

Waterston, R.

Direct Submission

Submitted (16-APR-2002) Department of Genetics, Washington

University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

On Mar 20, 2002 this sequence version replaced gi:18677559.

----- Genome Center

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc>

Contact: sapiens@watson.wustl.edu

----- Summary Statistics

Center project name: H_NH0030G07

NOTICE: This sequence may not represent the entire insert of this

clone. It may be shorter because we only sequence overlapping

clone sections once, or longer because we provide a small overlap

between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:

all regions were double stranded, sequenced with an alternate

chemistry, or covered by high quality data (i.e., phred quality >=

30); an attempt was made to resolve all sequencing problems, such

as compressions and repeats; all regions were covered by sequence

from more than one subclone; and the assembly was confirmed by

restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D.

McPherson, Department of Genetics, Washington University, St. Louis

MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPci-11 human BAC library was made from the blood of one male donor, as described by Ooegawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.regen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-549H5, 2000 bp overlap; the clone sequenced to the right is RP11-292K15, 2000 bp overlap. Actual start of this clone is at base position 161901 of RP11-549H5; actual end is at base position 18470 of RP11-292K15.

There are unresolved homopolymeric runs from 34720 to 34746 and 19405 to 19423.

FEATURES

source

Location/Qualifiers

1. .150010
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="2"
/map="2"

/clone="RP11-30G7"

/clone_lib="RPCi-11"

repeat_region

285. 476

/rpt_family="L2"

repeat_region

1269. 1382

/rpt_family="L1"

repeat_region

1396. 1561

/rpt_family="MER1_type"

repeat_region

1690. 1911

/rpt_family="L2"

repeat_region

2057. 2169

/rpt_family="MIR"

repeat_region

2382. 2515

/rpt_family="Alu"

repeat_region

2539. 2854

/rpt_family="Alu"

repeat_region

2855. 3148

/rpt_family="Alu"

repeat_region

3570. 3729

/rpt_family="L2"

repeat_region

3722. 3889

/rpt_family="MIR"

repeat_region

4843. 5031

/rpt_family="MIR"

repeat_region

5032. 5329

/rpt_family="Alu"

repeat_region

5330. 5376

/rpt_family="MIR"

repeat_region

5379. 5411

/rpt_family="CT-rich"

repeat_region

5412. 5436

/rpt_family="CA)n"

repeat_region

5737. 5958

/rpt_family="Alu"

repeat_region

6826. 7108

/rpt_family="Alu"

repeat_region

7115. 7206

/rpt_family="(GAAA)n"

repeat_region

7266. 7394

/rpt_family="Alu"

repeat_region

8707. 9660

/rpt_family="L1"

repeat_region

15756. 16206

/rpt_family="ERV1"

repeat_region

16207. 16509

repeat_region
16510. 16546
/rpt_family="ERV1"
repeat_region
16993. 17300
/rpt_family="Alu"
repeat_region
17936. 18404
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repeat_region
18567. 18724
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18754. 18773
/rpt_family="(CAA)n"
repeat_region
19159. 19255
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repeat_region
19402. 19424
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20101. 20407
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20459. 21137
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21269. 21502
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repeat_region
21624. 21927
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repeat_region
21949. 21973
/rpt_family="(CAAAA)n"
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21975. 22200
/rpt_family="L1"
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22201. 22518
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22519. 23041
/rpt_family="L1"
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23047. 23132
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23179. 23634
/rpt_family="L1"
repeat_region
23637. 23726
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repeat_region
23729. 24237
/rpt_family="MER2_type"
repeat_region
24243. 25648
/rpt_family="L1"
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25808. 25881
/rpt_family="L1"
repeat_region
25882. 25908
/rpt_family="(TG)n"
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25909. 26454
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repeat_region
26455. 27618
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27641. 28259
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28260. 28561
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28562. 29112
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29113. 29395
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repeat_region
29396. 30357
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Query Match 84.0%; Score 16.8; DB 9; Length 150010;
Best Local Similarity 90.0%; Pred.No.5.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGGCTCTCTGAGTAGCAG 20

|||||

Db 65730 AGGGAGTCTCTGAGAGCAG 65711

RESULT 47

AC133622

LOCUS

DEFINITION Rattus norvegicus clone CH230-380C8, *** SEQUENCING IN PROGRESS

150354 bp

DNA

linear

HTG 16-SEP-2002


```

***, 61 unordered pieces.
AC133622
AC133622.1 GI:22901964
HTG; HTGS PHASE1.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Mammalia; Eucarya; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eucarya; Chordata; Vertebrata; Euteleostomi;
Rattus.
1 (bases 1 to 150354)
Muzny, D. Marie., Metzker, M. Lee., Abramson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswal, K., Blair, J., Blankenburg, K., Blythe, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyie, M., Cree, A., D'Souza, L.,
Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escoto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
Gebregorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogue, M.,
Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A.,
Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
Liu, J., Liu, W., Liu, J., London, P., Longacre, S., Lopez, J.,
Lorensu, L., Loulseghe, H., Lozano, R. J., Lu, X., Ma, J.,
Maheshwari, M., Mahindrasekaran, M., Mahmoud, M., Martin, K., Mangum, A.,
Mangum, B., Mapua, P., Martin, K., Martin, K., Martinec, E.,
Mawhinney, S., McLeod, M., McNeill, T., Meenen, E., Milosavljevic, A.,
Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K.,
Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D.,
Newton, N., Nguyen, N., Norris, S., Nwankwelu, O., Okunolu, G.,
Olanrunso, A., Pal, S., Parks, K., Pasternak, S., Paul, H.,
Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A.,
Popovic, D., Primus, E., Pu, L., L., Puazo, M., Quiroz, J., Rachlin, E.,
Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y.,
Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A.,
Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Savary, G., Scherer, S.,
Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A.,
Sisson, I., Sitter, C. D., Smajic, D., Sneed, A., Sodergren, E.,
Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A.,
Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S.,
Tingey, A., Trejos, Z., Umani, K., Valas, R., Vera, V., Villaseana, D.,
Walton, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J.,
Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczky, R.,
Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S.,
Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X.,
Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D. R.,
Holt, R. A., Smith, H. O., Weinstein, G. and Gibbs, R. A.
Direct Submission
Unpublished
2 (bases 1 to 150354)
Rat Genome Sequencing Consortium.
Rat Genome Sequencing Consortium.
Submitted (16-SEP-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: KART

```

Center clone name: CH230-380C8
Sequencing vector: plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 105186 bases at least Q40
Consensus quality: 113495 bases at least Q30
Consensus quality: 118387 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 61 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1
1052: contig of 1052 bp in length
1152: gap of unknown length
1153: contig of 1496 bp in length
1153: gap of unknown length
2649: contig of 1325 bp in length
2749: contig of 1325 bp in length
4074: gap of unknown length
4174: contig of 1350 bp in length
5523: gap of unknown length
5524: contig of 1315 bp in length
6938: gap of unknown length
6939: contig of 2172 bp in length
7039: gap of unknown length
9211: contig of 1551 bp in length
9311: contig of 1551 bp in length
10861: gap of unknown length
10862: contig of 1612 bp in length
12574: gap of unknown length
12574: contig of 1137 bp in length
13810: gap of unknown length
13811: contig of 1411 bp in length
15322: gap of unknown length
15421: contig of 1379 bp in length
16800: gap of unknown length
16801: contig of 1299 bp in length
18200: gap of unknown length
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19569: gap of unknown length
19569: contig of 1140 bp in length
20809: gap of unknown length
20809: contig of 1069 bp in length
21977: gap of unknown length
21977: contig of 2256 bp in length
24333: gap of unknown length
24333: contig of 1801 bp in length
26234: gap of unknown length
26234: contig of 2487 bp in length
28821: gap of unknown length
28821: contig of 1742 bp in length
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30663: contig of 1522 bp in length
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3285: contig of 1695 bp in length
34080: gap of unknown length
34180: contig of 1499 bp in length
35779: gap of unknown length
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40357: gap of unknown length
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43365: gap of unknown length
43365: contig of 1597 bp in length
45062: gap of unknown length
45062: contig of 1807 bp in length
47069: gap of unknown length

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* 47070 49637: contig of 2568 bp in length
* 49638 49737: gap of unknown length
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* 53644 53743: gap of unknown length
* 53744 55353: contig of 1610 bp in length
* 55354 55453: gap of unknown length
* 55454 58176: contig of 2723 bp in length
* 58177 58276: gap of unknown length
* 58277 60664: contig of 2388 bp in length
* 60665 60764: gap of unknown length
* 60765 62799: contig of 2035 bp in length
* 62800 62899: gap of unknown length
* 62900 65808: contig of 2909 bp in length
* 65809 65908: gap of unknown length
* 65909 68722: contig of 2814 bp in length
* 68723 68822: gap of unknown length
* 68823 70990: contig of 2168 bp in length
* 70991 71090: gap of unknown length
* 71091 72739: contig of 1649 bp in length
* 72740 72839: gap of unknown length
* 72840 75263: contig of 2424 bp in length
* 75264 75363: gap of unknown length
* 75364 76380: contig of 1017 bp in length
* 76381 76480: gap of unknown length
* 76481 78500: contig of 2020 bp in length
* 78501 78600: gap of unknown length
* 78601 80836: contig of 2236 bp in length
* 80837 80936: gap of unknown length
* 80937 84694: contig of 3758 bp in length
* 84695 84794: gap of unknown length
* 84795 87092: contig of 2298 bp in length
* 87093 87192: gap of unknown length
* 87193 89597: contig of 2405 bp in length
* 89598 89697: gap of unknown length
* 89698 91675: contig of 1978 bp in length
* 91676 91775: gap of unknown length
* 91776 94065: contig of 2290 bp in length
* 94066 94165: gap of unknown length
* 94166 97567: contig of 3402 bp in length
* 97568 97667: gap of unknown length
* 97668 99859: contig of 2202 bp in length
* 99870 99959: gap of unknown length
* 99970 102460: contig of 2491 bp in length
* 102461 102560: gap of unknown length
* 102561 104482: contig of 1922 bp in length
* 104483 104582: gap of unknown length
* 104583 107242: contig of 2660 bp in length
* 107243 107342: gap of unknown length
* 107343 110239: contig of 2897 bp in length
* 110240 110339: gap of unknown length
* 110340 113361: contig of 3022 bp in length
* 113362 113461: gap of unknown length

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Query Match      84.0%; Score 16.8; DB 2; Length 150354;
Best Local Similarity 90.0%; Pred. No. 5 se+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 AGGGCGTCTCTGAGTAGCAG 20
    |||||
Db 66864 AGGGACTCACTGAGTAGCAG 66883

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RESULT 48
AC019258
LOCUS AC019258 155211 bp DNA linear HTG 13-JUL-2000
DEFINITION Homo sapiens clone RP11-2M23, LOW-PASS SEQUENCE SAMPLING.
ACCESSION AC019258
VERSION AC019258.2 GI:7209488
KEYWORDS HTG; HTGS_PHASE0.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE

```

1 (bases 1 to 155211)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-2M23
Unpublished
2 (bases 1 to 155211)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Bada,F.,
Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,A.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
DeArellano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J.,
Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J.,
Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G., Locke,K.,
Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
McPheeters,R., Meldrim,J., Meneus,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Olivari,T.M., Peterson,K.,
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
Zimmer,A. and Zody,M.
Direct Submission
Submitted (31-DEC-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 8, 2000 this sequence version replaced gi:6649456.
All repeats were identified using RepeatMasker:
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: W188
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L2672
Center clone name: 2_M_23
-----
* NOTE: This record contains 177 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
* 1 756: contig of 756 bp in length
* 757 856: gap of 100 bp
* 857 1619: contig of 763 bp in length
* 1620 1719: gap of 100 bp
* 1720 2498: contig of 779 bp in length
* 2499 2598: gap of 100 bp
* 2599 3355: contig of 757 bp in length
* 3356 3455: gap of 100 bp
* 3456 4201: contig of 746 bp in length
* 4202 4301: gap of 100 bp
* 4302 5053: contig of 752 bp in length
* 5054 5153: gap of 100 bp
* 5154 5910: contig of 757 bp in length
* 5911 6010: gap of 100 bp
* 6011 6779: contig of 769 bp in length
* 6780 6879: gap of 100 bp
* 6880 7629: contig of 750 bp in length
* 7630 7729: gap of 100 bp
* 7730 8485: contig of 756 bp in length
* 8486 8585: gap of 100 bp
* 8586 9348: contig of 763 bp in length
* 9349 9449: gap of 100 bp
* 9449 10225: contig of 777 bp in length
* 10226 10325: gap of 100 bp

```

TITLE

JOURNAL

COMMENT

* 10326 11083: contig of 758 bp in length
* 11084 11183: gap of 100 bp
* 11184 11964: contig of 781 bp in length
* 11965 12064: gap of 100 bp
* 12065 12830: contig of 766 bp in length
* 12831 12930: gap of 100 bp
* 12931 13692: contig of 762 bp in length
* 13693 13792: gap of 100 bp
* 13793 14557: contig of 765 bp in length
* 14558 14657: gap of 100 bp
* 14658 15412: contig of 755 bp in length
* 15413 15512: gap of 100 bp
* 15513 16282: contig of 770 bp in length
* 16283 16382: gap of 100 bp
* 16383 17131: contig of 749 bp in length
* 17132 17231: gap of 100 bp
* 17232 17980: contig of 749 bp in length
* 17981 18080: gap of 100 bp
* 18081 18839: contig of 759 bp in length
* 18840 18939: gap of 100 bp
* 18940 19701: contig of 762 bp in length
* 19702 19801: gap of 100 bp
* 19802 20565: contig of 764 bp in length
* 20566 20665: gap of 100 bp
* 20666 21415: contig of 750 bp in length
* 21416 21515: gap of 100 bp
* 21516 22286: contig of 771 bp in length
* 22287 22386: gap of 100 bp
* 22387 23161: contig of 775 bp in length
* 23162 23611: gap of 100 bp
* 23612 24022: contig of 761 bp in length
* 24023 24122: gap of 100 bp
* 24123 24872: contig of 750 bp in length
* 24873 24972: gap of 100 bp
* 24973 25554: contig of 682 bp in length
* 25555 25754: gap of 100 bp
* 25755 26510: contig of 756 bp in length
* 26511 27369: contig of 759 bp in length
* 27370 27469: gap of 100 bp
* 27470 28209: contig of 740 bp in length
* 28210 28309: gap of 100 bp
* 28310 29077: contig of 768 bp in length
* 29078 29177: gap of 100 bp
* 29178 29924: contig of 747 bp in length
* 29925 30024: gap of 100 bp
* 30025 30796: contig of 772 bp in length
* 30797 30896: gap of 100 bp
* 30897 31655: contig of 759 bp in length
* 31656 31755: gap of 100 bp
* 31756 32502: contig of 747 bp in length
* 32503 32602: gap of 100 bp
* 32603 33369: contig of 767 bp in length
* 33370 33470: gap of 100 bp
* 33470 34233: contig of 764 bp in length
* 34234 34333: gap of 100 bp
* 34334 35081: contig of 748 bp in length
* 35082 35181: gap of 100 bp
* 35182 35951: contig of 770 bp in length
* 35952 36051: gap of 100 bp
* 36052 36820: contig of 769 bp in length
* 36821 36920: gap of 100 bp
* 36921 37694: contig of 774 bp in length
* 37695 37794: gap of 100 bp
* 37795 38563: contig of 769 bp in length
* 38564 38663: gap of 100 bp
* 38664 39427: contig of 764 bp in length
* 39428 39527: gap of 100 bp
* 39528 40285: contig of 758 bp in length
* 40286 40385: gap of 100 bp
* 40386 41148: contig of 763 bp in length
* 41149 41248: gap of 100 bp
* 41249 42007: contig of 759 bp in length

* 42008 42107: gap of 100 bp
* 42108 42867: contig of 760 bp in length
* 42868 42967: gap of 100 bp
* 42968 43716: contig of 749 bp in length
* 43717 43816: gap of 100 bp
* 43817 44549: contig of 733 bp in length
* 44550 44649: gap of 100 bp
* 44650 45404: contig of 755 bp in length
* 45405 45504: gap of 100 bp
* 45505 46270: contig of 766 bp in length
* 46271 46370: gap of 100 bp
* 46371 47132: contig of 762 bp in length
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* 47233 48006: contig of 774 bp in length
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* 48107 48875: contig of 769 bp in length
* 48876 48975: gap of 100 bp
* 48976 49735: contig of 760 bp in length
* 49736 49835: gap of 100 bp
* 49836 50585: contig of 750 bp in length
* 50586 51449: contig of 764 bp in length
* 51450 51549: gap of 100 bp
* 51550 52306: contig of 757 bp in length
* 52307 52406: gap of 100 bp
* 52407 53158: contig of 752 bp in length
* 53159 53258: gap of 100 bp
* 53259 54002: contig of 744 bp in length
* 54003 54102: gap of 100 bp
* 54103 54883: contig of 781 bp in length
* 54884 54983: gap of 100 bp
* 54984 55748: contig of 765 bp in length
* 55749 55848: gap of 100 bp
* 55849 56621: contig of 773 bp in length
* 56622 56721: gap of 100 bp
* 56722 57477: contig of 756 bp in length
* 57478 57577: gap of 100 bp
* 57578 58335: contig of 758 bp in length
* 58336 58435: gap of 100 bp
* 58436 59188: contig of 753 bp in length
* 59189 59288: gap of 100 bp
* 59289 60050: contig of 762 bp in length
* 60051 60150: gap of 100 bp
* 60151 60905: contig of 755 bp in length
* 60906 61005: gap of 100 bp

Query Match 84.0%; Score 16.8; DB 2; Length 155211;
Best Local Similarity 90.0%; Pred. No. 5.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGGGCGTCTCGAGTAGCAG 20
Db 143745 ATGGCGTTCTCGAGTAGCAG 143764

RESULT 49

AC128702/c

LOCUS

DEFINITION

Mus musculus BAC clone RP24-239M3 from chromosome 9, complete

sequence.

AC128702

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 159431)

Dignan, G. and Cotton, M.

AUTHORS

TITLE

JOURNAL

REFERENCE

2 (bases 1 to 159431)

Unpublished (2001)

WILSON, R.

AC128702 159431 bp DNA linear ROD 13-NOV-2003
Mus musculus BAC clone RP24-239M3 from chromosome 9, complete

sequence.
AC128702

AC128702.4 GI:28604184

HTG

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 159431)

Dignan, G. and Cotton, M.

AUTHORS

TITLE

JOURNAL

REFERENCE

2 (bases 1 to 159431)

Unpublished (2001)

WILSON, R.


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repeat_region 17554..17717
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repeat_region 23167..23361
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repeat_region 23516..23591
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repeat_region 23596..23647
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Query Match 84.0%; Score 16.8; DB 10; Length 159431;

Best Local Similarity 90.0%; Pred.No. 5.5e+02; Mismatches 0; Gaps 0;

Matches 18; Conservative 0; Indels 0; Gaps 0;

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QY 1 AGGGCTCTCTGAGTAGCAG 20
Db 108672 AGGGCTCTCTGAGTAGCAG 108653

RESULT 50
AC053534/c
LOCUS
DEFINITION Homo sapiens chromosome 3 clone RP11-745B12, WORKING DRAFT
ACCESSION AC053534
VERSION AC053534.3 GI:13270837
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 160872)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 160872)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (16-APR-2000) Genome Sequencing Center, Washington
University School of Medicine, 444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Mar 10, 2001 this sequence version replaced gi:11496398.
----- Genome Center -----

```

```

Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@wustl.edu
----- Project Information -----
Center project name: H_NH0745B12
----- Summary Statistics -----
Sequencing vector: M13; 100%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 138905 bases at least Q40
Consensus quality: 146101 bases at least Q30
Consensus quality: 149339 bases at least Q20
Insert size: 175000; agarose-fp
Insert size: 156372; sum-of-contigs
Quality coverage: 2.92 in Q20 bases; agarose-fp
Quality coverage: 3.02 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 46 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1335: contig of 1335 bp in length
* 1336 1435: gap of unknown length
* 1436 2709: contig of 1274 bp in length
* 2710 2809: gap of unknown length
* 2810 4388: contig of 1579 bp in length
* 4389 4488: gap of unknown length
* 4489 5988: contig of 1500 bp in length
* 5989 6089: gap of unknown length
* 6090 8210: contig of 2022 bp in length
* 8211 9403: contig of 1193 bp in length
* 9404 9503: gap of unknown length
* 9504 10749: contig of 1246 bp in length
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* 10851 11851: contig of 1001 bp in length
* 11852 13665: gap of unknown length
* 13666 13764: gap of unknown length
* 13765 15351: contig of 1586 bp in length
* 15352 17052: contig of 1602 bp in length
* 17053 18810: contig of 1658 bp in length
* 18811 18910: gap of unknown length
* 18911 20642: contig of 1732 bp in length
* 20643 20742: gap of unknown length
* 20743 22067: contig of 1324 bp in length
* 22068 22167: gap of unknown length
* 22168 25000: contig of 2734 bp in length
* 25001 28018: contig of 3018 bp in length
* 28019 30655: contig of 2537 bp in length
* 30656 33140: contig of 2385 bp in length
* 33141 35367: contig of 2127 bp in length
* 35368 37817: gap of unknown length
* 37818 39518: contig of 2350 bp in length
* 39519 41065: contig of 3147 bp in length
* 41066 44644: contig of 3480 bp in length
* 44645 44744: gap of unknown length

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* 44745 47442: contig of 2698 bp in length
* 47443 47542: gap of unknown length
* 47543 49411: contig of 1869 bp in length
* 49412 49511: gap of unknown length
* 49512 52288: contig of 2777 bp in length
* 52289 52389: gap of unknown length
* 52389 55771: contig of 3383 bp in length
* 55772 55871: gap of unknown length
* 55872 58117: contig of 2246 bp in length
* 58118 58217: gap of unknown length
* 58218 61622: contig of 3405 bp in length
* 61623 61722: gap of unknown length
* 61723 65588: contig of 3866 bp in length
* 65589 65688: gap of unknown length
* 65689 69895: contig of 4207 bp in length
* 69896 69995: gap of unknown length
* 69996 72794: contig of 2798 bp in length
* 72794 72893: gap of unknown length
* 72894 75602: contig of 2709 bp in length
* 75603 75703: gap of unknown length
* 75703 79092: contig of 3390 bp in length
* 79093 79192: gap of unknown length
* 79193 83380: contig of 4188 bp in length
* 83381 83480: gap of unknown length
* 83481 86497: contig of 3017 bp in length
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* 86598 89889: contig of 3292 bp in length
* 89890 93787: gap of unknown length
* 93788 93887: contig of 3798 bp in length
* 93888 97050: contig of 3163 bp in length
* 97051 97150: gap of unknown length
* 97151 100721: contig of 3571 bp in length
* 100722 100821: gap of unknown length
* 100822 106757: contig of 5936 bp in length
* 106758 106857: gap of unknown length
* 106858 113422: contig of 5565 bp in length
* 113423 113523: gap of unknown length
* 113523 121377: contig of 7855 bp in length
* 121378 121477: gap of unknown length
* 121478 130444: contig of 8967 bp in length
* 130445 139345: contig of 8801 bp in length
* 139346 139446: gap of unknown length
* 139446 148719: contig of 9274 bp in length
* 148720 148819: gap of unknown length
* 148820 160872: contig of 12053 bp in length.

FEATURES

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="3"
/clone="RP11-745B12"

misc_feature 1..1335
/note="assembly_name:Contig12"
misc_feature 1436..2709
/note="assembly_name:Contig13"
misc_feature 2810..4388
/note="assembly_name:Contig15"
misc_feature 4489..5988
/note="assembly_name:Contig16"
misc_feature 6089..8110
/note="assembly_name:Contig17"
misc_feature 8211..9403
/note="assembly_name:Contig18"
misc_feature 9504..10749
/note="assembly_name:Contig19"
misc_feature 10850..11850
/note="assembly_name:Contig2"
misc_feature 11951..13664
/note="assembly_name:Contig20"
misc_feature 13765..15350

misc_feature /note="assembly_name:Contig22"
15451..17052
/note="assembly_name:Contig23"
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/note="assembly_name:Contig24"
18911..20642
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20743..22066
/note="assembly_name:Contig26"
22167..24900
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25001..28018
/note="assembly_name:Contig28"
28119..30655
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30756..33140
/note="assembly_name:Contig30"
33241..35367
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35468..37817
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37918..41064
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41165..44644
/note="assembly_name:Contig34"
44745..47442
/note="assembly_name:Contig35"
47543..49411
/note="assembly_name:Contig36"
49512..52288
/note="assembly_name:Contig37"

Query Match 84.0%; Score 16.8; DB 2; Length 160872;
Best Local Similarity 90.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
|||||
DB 153066 AGGGATTCCTGAGTAGCAG 153047

Search completed: March 14, 2005, 20:42:21
Job time : 1794 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 14, 2005, 17:14:02 ; Search time 252 Seconds
(without alignments)
469.821 Million cell updates/sec

Title: US-10-672-399-10

Perfect score: 20

Sequence: 1 agggcgtctctgagtagcag 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : N_Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	100.0	1737	10 ADL13691	Adl13691 Osteoarth
C 2	20	100.0	1737	10 ADL13692	Adl13692 Osteoarth
C 3	20	100.0	2087	10 ADL13694	Adl13694 Osteoarth
C 4	20	100.0	2088	10 ADL13690	Adl13690 Osteoarth
C 5	20	100.0	2116	2 AAT99541	Aat99541 Human hya
C 6	20	100.0	2117	2 AAT96713	Aat96713 Human hya
C 7	20	100.0	23122	10 ADL13693	Adl13693 Osteoarth
C 8	17.4	87.0	1752	8 ABZ76734	Abz76734 Mouse hya
C 9	17.4	87.0	1752	10 AAD59442	Aad59442 Mouse hya
C 10	17.4	87.0	2102	2 AAT91655	Aat91655 Mouse hya
C 11	17.4	87.0	2102	2 AAZ10862	Aaz10862 Hyalurona
C 12	17.4	87.0	2102	3 AAZ88199	Aaz88199 Mouse hya
C 13	17.4	87.0	2102	3 AAA39987	Aaa39987 Murine HA
C 14	16.8	84.0	239	12 ACH89039	Ach89039 Human gen
C 15	16.8	84.0	278	3 AAC10010	Aac10010 Human sec
C 16	16.8	84.0	313	3 AAC0292	Aac0292 Human sec
C 17	16.8	84.0	595	12 ACH75339	Ach75339 Human gen
C 18	16.8	84.0	775	5 AAH19499	Aah19499 Human gal
C 19	16.8	84.0	80105	13 ABD33213	Abd33213 Murine ca
C 20	16.4	82.0	300	2 AAX98492	Aax98492 Human can

21	16.4	82.0	452	2 AAX99116	Aax99116 Human can
C 22	16.4	82.0	748	12 ADJ42940	Adj42940 Plant CDN
C 23	16.4	82.0	1611	10 ADB62940	Adb62940 Human CDN
24	16.4	82.0	1992	3 AAC77862	Aac77862 Human can
25	16.4	82.0	2057	4 AAH17632	Aah17632 Human CDN
26	16.4	82.0	2250	10 ADF83544	Adf83544 Human GRI
C 27	16.4	82.0	2508	13 ACN37249	Acn37249 Tumour-as
C 28	16.4	82.0	2665	6 ABL90233	AbL90233 Human pol
29	16.4	82.0	2753	4 AAH18559	Aah18559 Human CDN
C 30	16.4	82.0	2781	3 AAH72382	Aah72382 Human nuc
C 31	16.4	82.0	3163	4 AAK52536	Aak52536 Human pol
C 32	16.4	82.0	3236	4 AAK51552	Aak51552 Human pol
C 33	16.4	82.0	3619	3 AAK75812	Aac75812 Human ORF
C 34	16.4	82.0	4560	12 ADQ23383	Adq23383 Human eof
C 35	16.4	82.0	15105	10 ADF83532	Adf83532 Human GRI
C 36	16.4	82.0	63411	12 ADQ97081	Adq97081 Mouse can
C 37	15.8	79.0	458	9 ACH41376	Ach41376 Human foe
C 38	15.8	79.0	525	4 AAH22902	Aah22902 Codon opt
C 39	15.8	79.0	525	10 ABD41220	Abd41220 DNA encod
C 40	15.8	79.0	531	6 ABS2517	AbS2517 DNA encod
C 41	15.8	79.0	596	8 AB253961	Abz53961 Aspergill
C 42	15.8	79.0	779	3 AAA01703	Aaa01703 Human col
C 43	15.8	79.0	882	11 ABD12260	Abd12260 Pseudomon
C 44	15.8	79.0	1203	11 ABD12216	Abd12216 Pseudomon
C 45	15.8	79.0	2069	13 ADR07772	Adr07772 Full leng
C 46	15.8	79.0	2614	2 AAV48219	Aav48219 Mouse str
C 47	15.8	79.0	2614	3 AAZ51045	Aaz51045 Mouse str
C 48	15.8	79.0	2928	12 ADQ97808	Adq97808 Mouse can
C 49	15.8	79.0	5000	4 AAS14505	Aas14505 Human GST
C 50	15.8	79.0	5727	10 ADK40991	Adk40991 Novel hum
C 51	15.8	79.0	5727	13 ADR15705	Adr15705 Kinase 41
C 52	15.8	79.0	5823	4 AAF22450	Aaf22450 Human bre
C 53	15.8	79.0	5866	8 ACC72055	Acc72055 BCU0518 g
C 54	15.8	79.0	6413	4 AAK52956	Aak52956 Human pol
C 55	15.8	79.0	6418	4 AAK51372	Aak51372 Human pol
C 56	15.8	79.0	6440	13 ACN39118	Acn39118 Tumour-as
C 57	15.8	79.0	47040	12 ADQ97807	Adq97807 Mouse can
C 58	15.8	79.0	53795	9 ADA02858	Ada02858 Human LMO
C 59	15.8	79.0	53795	10 ADB72596	Adb72596 Human LMO
C 60	15.8	79.0	53795	10 ADC85337	Adc85337 Mouse Lmo
C 61	15.8	79.0	53795	12 ADM74453	Adm74453 Human car
C 62	15.8	79.0	73465	6 ABQ88161	Abq88161 Human oet
C 63	15.8	79.0	110000	4 AAI99682_04	Continuation (5 of
C 64	15.8	79.0	110000	4 AAI99683_04	Continuation (5 of
C 65	15.8	79.0	114793	4 AAD08215	Aad08215 Human gen
C 66	15.8	79.0	153170	12 ADQ17382	Adq17382 Human sof
C 67	15.8	79.0	208765	12 ADQ97430	Adq97430 Mouse can
C 68	15.4	77.0	433	3 AAF08984	Aaf08984 Fusarium
C 69	15.4	77.0	433	8 ABX64635	Abx64635 Human gen
C 70	15.4	77.0	962	6 ABL39698	AbL39698 Human NS
C 71	15.4	77.0	1066	4 AAS22818	Aas22818 Human CDN
C 72	15.4	77.0	1066	13 ADS11519	AdS11519 Human the
C 73	15.4	77.0	1255	4 AAS22582	Aas22582 Human CDN
C 74	15.4	77.0	1285	6 AAD36080	Aad36080 Human ATP
C 75	15.4	77.0	1285	6 AAD36081	Aad36081 Human ATP
C 76	15.4	77.0	2016	13 ACN37559	Acn37559 Tumour-as
C 77	15.4	77.0	2074	2 AAX04354	Aax04354 Human sec
C 78	15.4	77.0	15843	11 ACN44786	Acn44786 Human gen
C 79	15.2	76.0	21	13 ADS18343	AdS18343 Murine TR
C 80	15.2	76.0	159	4 AAI55222	Aai55222 Probe #23
C 81	15.2	76.0	159	4 ABS48980	AbS48980 Human liv
C 82	15.2	76.0	380	12 ADP93531	Adp93531 Cotton ex
C 83	15.2	76.0	498	9 ACH36536	Ach36536 Human end
C 84	15.2	76.0	499	3 AAC00811	Aac00811 Human sec
C 85	15.2	76.0	503	9 ACH33753	Ach33753 Human end
C 86	15.2	76.0	548	5 AAS45111	Aas45111 cDNA enco
C 87	15.2	76.0	554	4 AAI43036	Aai43036 Probe #11
C 88	15.2	76.0	554	4 ABS36880	AbS36880 Human liv
C 89	15.2	76.0	563	8 ABS253427	AbS253427 Aspergill
C 90	15.2	76.0	574	13 ADQ58168	AdQ58168 Novel can
C 91	15.2	76.0	606	11 ABD02003	Abd02003 Pseudomon
C 92	15.2	76.0	684	10 ADJ32129	Adj32129 Human int
C 93	15.2	76.0	744	10 ADF58008	Adf58008 Human pol

C 94	15.2	76.0	834	6	AAD27736	Aad27736 Human ful
C 95	15.2	76.0	895	6	AAD29597	Aad29597 Human cdn
C 96	15.2	76.0	910	12	AD035687	Ad035687 Novel mou
C 97	15.2	76.0	960	4	ABL08433	AbL08433 Drosophill
C 98	15.2	76.0	1077	10	Ade29368	Ade29368 Human ser
C 99	15.2	76.0	1078	4	AAP83972	Aaf83972 Nucleotid
C 100	15.2	76.0	1101	12	ADH17419	Adh17419 Human NOV
C 101	15.2	76.0	1110	12	ADH17423	Adh17423 Human NOV
C 102	15.2	76.0	1146	12	ADH17443	Adh17443 Human NOV
C 103	15.2	76.0	1182	11	ABD01916	Abd01916 Pseudomon
C 104	15.2	76.0	1203	12	ADH17425	Adh17425 Human NOV
C 105	15.2	76.0	1203	12	ADH17421	Adh17421 Human NOV
C 106	15.2	76.0	1203	12	ADH17427	Adh17427 Human NOV
C 107	15.2	76.0	1218	12	ADH17435	Adh17435 Human NOV
C 108	15.2	76.0	1218	12	ADH17447	Adh17447 Human NOV
C 109	15.2	76.0	1230	6	AAD27743	Aad27743 Human tra
C 110	15.2	76.0	1282	10	ADE79051	Ade79051 Human pro
C 111	15.2	76.0	1299	11	ABD01892	Abd01892 Pseudomon
C 112	15.2	76.0	1314	4	AAP83973	Aaf83973 Nucleotid
C 113	15.2	76.0	1314	4	AAP83971	Aaf83971 Human SER
C 114	15.2	76.0	1314	10	ADE29366	Ade29366 Human cdn
C 115	15.2	76.0	1314	10	ADE29369	Ade29369 Human ser
C 116	15.2	76.0	1314	12	ADH17441	Adh17441 Human NOV
C 117	15.2	76.0	1341	8	ABZ22865	Abz22865 Human den
C 118	15.2	76.0	1407	10	ADE79039	Ade79039 Human pro
C 119	15.2	76.0	1409	10	ADE79066	Ade79066 Human pro
C 120	15.2	76.0	1434	8	ABZ22864	Abz22864 Human den
C 121	15.2	76.0	1448	10	ADE79040	Ade79040 Human pro
C 122	15.2	76.0	1568	8	ACC46449	Acc46449 Human dit
C 123	15.2	76.0	1574	6	AD30575	Ad30575 Human pro
C 124	15.2	76.0	1614	6	ABK31708	Abk31708 DNA encod
C 125	15.2	76.0	1626	12	ADH17431	Adh17431 Human NOV
C 126	15.2	76.0	1689	4	AAD05796	Aad05796 Human tra
C 127	15.2	76.0	1689	10	AD10392	Adi10392 Human cel
C 128	15.2	76.0	1689	12	ADJ46916	Adj46916 Human tra
C 129	15.2	76.0	1707	12	ADH17439	Adh17439 Human NOV
C 130	15.2	76.0	1708	12	ADH17457	Adh17457 Human NOV
C 131	15.2	76.0	1748	6	AAD27734	Aad27734 Human tra
C 132	15.2	76.0	1771	12	ADH17433	Adh17433 Human NOV
C 133	15.2	76.0	1779	12	ADH17429	Adh17429 Human NOV
C 134	15.2	76.0	1858	2	AAQ56202	Aaq56202 Partial c
C 135	15.2	76.0	1858	2	AAQ90126	Aaq90126 Plasmid p
C 136	15.2	76.0	1858	2	AT384418	At384418 pCK1 cDNA
C 137	15.2	76.0	1889	4	ABL12039	AbL12039 Drosophill
C 138	15.2	76.0	2057	4	AAD05797	Aad05797 Human tra
C 139	15.2	76.0	2067	10	AD10394	Adi10394 Human cel
C 140	15.2	76.0	2067	12	ADJ46918	Adj46918 Human tra
C 141	15.2	76.0	2192	4	AAH14850	Aah14850 Human cdn
C 142	15.2	76.0	2237	4	ABL23356	AbL23356 Drosophill
C 143	15.2	76.0	2310	12	ADH17437	Adh17437 Human NOV
C 144	15.2	76.0	2360	10	ADE79041	Ade79041 Human pro
C 145	15.2	76.0	2393	10	ADE31742	Ade31742 Human 291
C 146	15.2	76.0	2410	6	ABK12897	Abk12897 Human pro
C 147	15.2	76.0	2432	12	ADH17453	Adh17453 Human NOV
C 148	15.2	76.0	2432	12	ADH17451	Adh17451 Human NOV
C 149	15.2	76.0	2432	12	ADH17449	Adh17449 Human NOV
C 150	15.2	76.0	2432	12	ADH17413	Adh17413 Human NOV
C 151	15.2	76.0	2643	3	AAA46557	Aaa46557 cDNA sequ
C 152	15.2	76.0	2643	6	ABK72680	Abk72680 DNA encod
C 153	15.2	76.0	2682	13	ADR10444	Adr10444 Full leng
C 154	15.2	76.0	2727	5	AAS44923	Aas44923 cDNA enco
C 155	15.2	76.0	2865	4	ABL04669	AbL04669 Drosophill
C 156	15.2	76.0	3103	13	ACN42023	Acn42023 Human dia
C 157	15.2	76.0	3244	4	ABL08432	AbL08432 Drosophill
C 158	15.2	76.0	3472	4	ABL07626	AbL07626 Drosophill
C 159	15.2	76.0	4001	10	ADF18694	Adf18694 Human reg
C 160	15.2	76.0	4219	4	ABL04902	AbL04902 Drosophill
C 161	15.2	76.0	5110	6	ABL12038	AbL12038 Drosophill
C 162	15.2	76.0	5728	6	ABK62572	Abk62572 Rat sequ
C 163	15.2	76.0	5775	10	ADB58556	AdB58556 Toxicity-
C 164	15.2	76.0	5775	10	ADB53170	AdB53170 Primary r
C 165	15.2	76.0	6164	4	ABL04668	AbL04668 Drosophill
C 166	15.2	76.0	7513	10	ADC86982	Adc86982 Human GPC

C 167	15.2	76.0	15515	8	AAL53548	Aal53548 Genomic D
C 168	15.2	76.0	25083	9	ADA02855	Ada02855 Mouse lmo
C 169	15.2	76.0	25083	10	ADB72593	AdB72593 Mouse lmo
C 170	15.2	76.0	25083	10	ADC85334	Adc85334 Mouse Cbx
C 171	15.2	76.0	25083	12	ADM74450	Adm74450 Murine ca
C 172	15.2	76.0	25231	4	AAL03112	Aal03112 Human rep
C 173	15.2	76.0	49914	13	ABD33262	Abd33262 Murine ca
C 174	15.2	76.0	63248	11	ACN45100	Acn45100 Mouse gen
C 175	15.2	76.0	79640	13	ABD33007	Abd33007 Mouse can
C 176	15.2	76.0	112190	4	AHH44801	Aah44801 Human GPC
C 177	15.2	76.0	120144	13	ABD33161	Abd33161 Murine ca
C 178	15.2	76.0	129017	12	ADP84158	Adp84158 Human AST
C 179	15.2	76.0	150085	13	ABD32809	Abd32809 Mouse can
C 180	15.2	76.0	173810	6	ABN85752	Abn85752 Mouse chr
C 181	15.2	76.0	247509	10	ADL13684	Adl13684 Osteoarth
C 182	15	75.0	456	9	ACH33386	Ach33386 Human end
C 183	15	75.0	552	12	ACH78684	Ach78684 Human gen
C 184	15	75.0	1379	4	AAS22470	Aas22470 Human cdn
C 185	15	75.0	10622	4	AAK68203	Aak68203 Human imm
C 186	15	75.0	11876	12	ADQ18981	Adq18981 Human sof
C 187	15	75.0	11919	12	ADQ23338	Adq23338 Human sof
C 188	15	75.0	56743	4	AAK68202	Aak68202 Human imm
C 189	15	75.0	56743	4	AAK81760	Aak81760 Human imm
C 190	15	75.0	65464	8	ABX13172	Abx13172 Human gen
C 191	15	75.0	200418	11	ACN44226	Acn44226 Human gen
C 192	14.8	74.0	295	2	AAZ27708	Aaz27708 Human DNA
C 193	14.8	74.0	411	9	ACH17071	Ach17071 Human adu
C 194	14.8	74.0	455	9	ACH40376	Ach40376 Human foe
C 195	14.8	74.0	467	4	AAI11592	Aai11592 Probe #15
C 196	14.8	74.0	467	4	ABA53281	Abas53281 Human foe
C 197	14.8	74.0	467	4	AAI32884	Aai32884 Probe #15
C 198	14.8	74.0	467	4	ABA42858	Abas42858 Human bre
C 199	14.8	74.0	467	4	ABA23055	Abas23055 Probe #15
C 200	14.8	74.0	467	4	AAK26984	Aak26984 Human bon
C 201	14.8	74.0	467	4	AAK01539	Aak01539 Human bra
C 202	14.8	74.0	467	4	ABS26572	Abs26572 Human liv
C 203	14.8	74.0	467	5	AAI01516	Aai01516 Probe #15
C 204	14.8	74.0	467	6	ABS01571	Abs01571 Human gen
C 205	14.8	74.0	491	3	AAO07469	Aao07469 Human sec
C 206	14.8	74.0	513	6	ABN19118	Abn19118 Human ORF
C 207	14.8	74.0	552	10	ADD29823	Add29823 Human tum
C 208	14.8	74.0	572	4	AAI20806	Aai20806 Probe #10
C 209	14.8	74.0	572	4	ABA65874	Abas65874 Human foe
C 210	14.8	74.0	572	4	AAI46037	Aai46037 Probe #14
C 211	14.8	74.0	572	4	ABA47987	Abas47987 Human bre
C 212	14.8	74.0	572	4	ABA32960	Abas32960 Probe #11
C 213	14.8	74.0	572	4	AAK40017	Aak40017 Human bon
C 214	14.8	74.0	572	4	AAK14286	Aak14286 Human bra
C 215	14.8	74.0	572	4	ABS39603	Abs39603 Human liv
C 216	14.8	74.0	572	5	AAI06514	Aai06514 Probe #65
C 217	14.8	74.0	572	6	ABS14103	Abs14103 Human gen
C 218	14.8	74.0	660	12	ADL81735	Adl81735 P. aerugi
C 219	14.8	74.0	707	12	ADJ42941	Adj42941 Plant cdn
C 220	14.8	74.0	723	3	AAF12135	Aaf12135 Aspergill
C 221	14.8	74.0	774	11	ABD11205	Abd11205 Pseudomon
C 222	14.8	74.0	785	12	ADJ33613	Adj33613 Plant cdn
C 223	14.8	74.0	878	4	AAK93648	Aak93648 Human cdn
C 224	14.8	74.0	878	4	AAK91982	Aak91982 Human cdn
C 225	14.8	74.0	878	12	ADL30075	Adl30075 3' end of
C 226	14.8	74.0	878	12	ADL28409	Adl28409 5' end of
C 227	14.8	74.0	884	2	AAK99070	Aak99070 Human val
C 228	14.8	74.0	1002	8	ADA69388	Ada69388 Rice gene
C 229	14.8	74.0	1037	4	ABL10383	AbL10383 Drosophill
C 230	14.8	74.0	1089	11	ABD11386	Abd11386 Pseudomon
C 231	14.8	74.0	1158	3	AAS292421	Aas292421 DNA encod
C 232	14.8	74.0	1158	10	ACA62465	AcA62465 DNA encod
C 233	14.8	74.0	1168	6	ABS65599	Abs65599 Mouse gen
C 234	14.8	74.0	1254	2	AAI43482	Aat43482 ATM gene
C 235	14.8	74.0	1389	5	AAF57634	Aaf57634 ATM genom
C 236	14.8	74.0	1465	5	AAS87543	Aas87543 DNA encod
C 237	14.8	74.0	1465	5	AAS91285	Aas91285 DNA encod
C 238	14.8	74.0	1511	5	AAS89099	Aas89099 DNA encod
C 239	14.8	74.0	1537	6	ABV77431	Abv77431 Human syn

c 240	14.8	74.0	1560	2	AAQ54050	Human bon	313	14.8	74.0	9169	2	AAT68760	Aat68760	ATM	mutan
c 241	14.8	74.0	1640	2	AAT45868	Human bon	314	14.8	74.0	9169	2	AAT73811	Aat73811	ATM	gene
c 242	14.8	74.0	2000	10	ACC60866	Gene sequ	315	14.8	74.0	9169	2	AAT73808	Aat73808	ATM	gene
c 243	14.8	74.0	2000	10	ACC62245	Disease t	316	14.8	74.0	9170	2	AAT68762	Aat68762	ATM	mutan
c 244	14.8	74.0	2007	5	AS588300	DNA encod	317	14.8	74.0	9171	2	AAT68764	Aat68764	ATM	mutan
c 245	14.8	74.0	2245	8	ACC79893	Human DEL	318	14.8	74.0	9171	2	AAT68765	Aat68765	ATM	mutan
c 246	14.8	74.0	2271	11	ADJ11513	Rice DNA	319	14.8	74.0	9171	2	AAT68773	Aat68773	ATM	mutan
c 247	14.8	74.0	2484	11	ADM02858	Human cdn	320	14.8	74.0	9171	2	AAT68781	Aat68781	ATM	mutan
c 248	14.8	74.0	2532	11	ADN39337	Cancer/an	321	14.8	74.0	9171	2	AAT68768	Aat68768	ATM	mutan
c 249	14.8	74.0	2674	11	ADQ23720	Human sof	322	14.8	74.0	9171	2	AAT68782	Aat68782	ATM	mutan
c 250	14.8	74.0	2691	12	ADE15656	Human str	323	14.8	74.0	9171	2	AAT43497	ATM	open	
c 251	14.8	74.0	3012	11	ADM03028	Human cdn	324	14.8	74.0	9171	2	AAT68733	ATM	mutan	
c 252	14.8	74.0	3142	10	ADE56315	Human gen	325	14.8	74.0	9171	2	AAT45419	Ataxia-te		
c 253	14.8	74.0	3142	10	ADE56319	Human gen	326	14.8	74.0	9171	2	AAT73810	ATM	gene	
c 254	14.8	74.0	3142	10	ADD46110	Human gen	327	14.8	74.0	9171	2	AAT73810	ATM	gene	
c 255	14.8	74.0	3238	4	AAK94339	Human ful	328	14.8	74.0	9171	4	AAF57591	ATM	gene	
c 256	14.8	74.0	3238	4	AAK94339	Human ful	329	14.8	74.0	9171	4	AAD21841	Human	ATM	
c 257	14.8	74.0	3238	12	ADL31002	Full leng	330	14.8	74.0	9171	4	AAD21843	Human	ATM	
c 258	14.8	74.0	3408	8	AAU52899	Mouse two	331	14.8	74.0	9171	4	AAD21871	Human	ATM	
c 259	14.8	74.0	3495	13	ACN41849	Human dia	332	14.8	74.0	9171	4	AAD21836	Human	ATM	
c 260	14.8	74.0	3589	8	ABT32175	Human neu	333	14.8	74.0	9171	4	AAD21846	Human	ATM	
c 261	14.8	74.0	5080	8	ACD13351	Human DNA	334	14.8	74.0	9171	4	AAD21840	Human	ATM	
c 262	14.8	74.0	5912	2	AAT43519	ATM gene	335	14.8	74.0	9171	4	AAD21848	Human	ATM	
c 263	14.8	74.0	5912	2	AAT45423	Partial A	336	14.8	74.0	9171	4	AAD21853	Human	ATM	
c 264	14.8	74.0	5912	4	AAF57590	Nucleotid	337	14.8	74.0	9171	4	AAD21837	Human	ATM	
c 265	14.8	74.0	6487	8	ABZ74409	Secreted	338	14.8	74.0	9171	4	AAD21838	Human	ATM	
c 266	14.8	74.0	6487	8	ADA98861	Human sec	339	14.8	74.0	9171	4	AAD21845	Human	ATM	
c 267	14.8	74.0	6487	8	ADA44475	Human sec	340	14.8	74.0	9171	4	AAD21847	Human	ATM	
c 268	14.8	74.0	6487	10	ABZ67966	Human sec	341	14.8	74.0	9171	4	AAD21851	Human	ATM	
c 269	14.8	74.0	7207	6	ABU54575	Mouse per	342	14.8	74.0	9171	4	AAD21842	Human	ATM	
c 270	14.8	74.0	8341	2	AAT68772	ATM mutan	343	14.8	74.0	9171	4	AAD21850	Human	ATM	
c 271	14.8	74.0	8382	4	AAK70731	Human imm	344	14.8	74.0	9171	4	AAD21849	Human	ATM	
c 272	14.8	74.0	8682	4	ABU10382	Drosophil	345	14.8	74.0	9171	4	AAD21856	Human	ATM	
c 273	14.8	74.0	8712	5	AAH24106	Mouse Per	346	14.8	74.0	9171	4	AAD21834	Human	ATM	
c 274	14.8	74.0	8767	2	AAT68735	ATM mutan	347	14.8	74.0	9171	4	AAD21852	Human	ATM	
c 275	14.8	74.0	8768	2	AAT73812	ATM gene	348	14.8	74.0	9171	4	AAD21832	Human	ATM	
c 276	14.8	74.0	8799	2	AAT68758	ATM mutan	349	14.8	74.0	9171	4	AAD21872	Human	ATM	
c 277	14.8	74.0	8816	2	AAT68750	ATM mutan	350	14.8	74.0	9171	4	AAD21855	Human	ATM	
c 278	14.8	74.0	8873	2	AAT68740	ATM mutan	351	14.8	74.0	9171	4	AAD21831	Human	ATM	
c 279	14.8	74.0	8970	2	AAT68771	ATM mutan	352	14.8	74.0	9171	4	AAD21835	Human	ATM	
c 280	14.8	74.0	8996	2	AAT68754	ATM mutan	353	14.8	74.0	9171	4	AAD21844	Human	ATM	
c 281	14.8	74.0	8996	2	AAT68783	ATM mutan	354	14.8	74.0	9171	4	AAD21854	Human	ATM	
c 282	14.8	74.0	8997	2	AAT68756	ATM mutan	355	14.8	74.0	9171	4	AAD21780	Human	ATM	
c 283	14.8	74.0	8997	2	AAT68774	ATM mutan	356	14.8	74.0	9171	4	AAD21833	Human	ATM	
c 284	14.8	74.0	9006	2	AAT68775	ATM mutan	357	14.8	74.0	9171	4	AAD21839	Human	ATM	
c 285	14.8	74.0	9006	2	AAT68753	ATM mutan	358	14.8	74.0	9171	10	ADH68996	ATM	gene	
c 286	14.8	74.0	9012	2	AAT68741	ATM mutan	359	14.8	74.0	9171	10	ADH69001	ATM	gene	
c 287	14.8	74.0	9018	2	AAT68736	ATM mutan	360	14.8	74.0	9171	10	ADH68992	ATM	gene	
c 288	14.8	74.0	9022	2	AAT68745	ATM mutan	361	14.8	74.0	9171	10	ADH68997	ATM	gene	
c 289	14.8	74.0	9029	2	AAT68752	ATM mutan	362	14.8	74.0	9171	10	ADH68999	ATM	gene	
c 290	14.8	74.0	9032	2	AAT68739	ATM mutan	363	14.8	74.0	9171	10	ADH68989	ATM	gene	
c 291	14.8	74.0	9044	2	AAT68755	ATM mutan	364	14.8	74.0	9171	10	ADH68988	ATM	gene	
c 292	14.8	74.0	9046	2	AAT68770	ATM mutan	365	14.8	74.0	9171	10	ADH69004	Human	ATM	
c 293	14.8	74.0	9046	2	AAT68761	ATM mutan	366	14.8	74.0	9171	10	ADH69011	Human	ATM	
c 294	14.8	74.0	9066	2	AAT68744	ATM mutan	367	14.8	74.0	9171	10	ADH69013	Human	ATM	
c 295	14.8	74.0	9081	2	AAT68759	ATM mutan	368	14.8	74.0	9171	10	ADH69007	Human	ATM	
c 296	14.8	74.0	9088	2	AAT68757	ATM mutan	369	14.8	74.0	9171	10	ADH69008	Human	ATM	
c 297	14.8	74.0	9160	2	AAT68749	ATM mutan	370	14.8	74.0	9171	10	ADH69010	Human	ATM	
c 298	14.8	74.0	9162	2	AAT68777	ATM mutan	371	14.8	74.0	9171	10	ADH69012	Human	ATM	
c 299	14.8	74.0	9164	2	AAT68751	ATM mutan	372	14.8	74.0	9171	10	ADH68990	ATM	gene	
c 300	14.8	74.0	9165	2	AAT68785	ATM mutan	373	14.8	74.0	9171	10	ADH68993	ATM	gene	
c 301	14.8	74.0	9165	2	AAT68778	ATM mutan	374	14.8	74.0	9171	10	ADH68995	ATM	gene	
c 302	14.8	74.0	9166	2	AAT68746	ATM mutan	375	14.8	74.0	9171	10	ADH69006	Human	ATM	
c 303	14.8	74.0	9166	2	AAT68738	ATM mutan	376	14.8	74.0	9171	10	ADH68932	Human	ATM	
c 304	14.8	74.0	9166	2	AAT68743	ATM mutan	377	14.8	74.0	9171	10	ADH69000	ATM	gene	
c 305	14.8	74.0	9167	2	AAT68742	ATM mutan	378	14.8	74.0	9171	10	ADH68986	Human	ATM	
c 306	14.8	74.0	9167	2	AAT68769	ATM mutan	379	14.8	74.0	9171	10	ADH68998	ATM	gene	
c 307	14.8	74.0	9168	2	AAT68776	ATM mutan	380	14.8	74.0	9171	10	ADH69003	ATM	gene	
c 308	14.8	74.0	9168	2	AAT68780	ATM mutan	381	14.8	74.0	9171	10	ADH69002	ATM	gene	
c 309	14.8	74.0	9169	2	AAT68731	ATM mutan	382	14.8	74.0	9171	10	ADH69005	Human	ATM	
c 310	14.8	74.0	9169	2	AAT68763	ATM mutan	383	14.8	74.0	9171	10	ADH69009	Human	ATM	
c 311	14.8	74.0	9169	2	AAT68734	ATM mutan	384	14.8	74.0	9171	10	ADH68987	Human	ATM	
c 312	14.8	74.0	9169	2	AAT68766	ATM mutan	385	14.8	74.0	9171	10	ADH68991	ATM	gene	

386	14.8	74.0	9171	10	ADH68994	Adh68994	ATM gene	459	14.8	74.0	90351	13	ABD32651	Abd32651	Mouse can
387	14.8	74.0	9172	2	AAT68747	Aat68747	ATM mutan	c 460	14.8	74.0	90351	13	ABD32651	Abd32651	Mouse can
388	14.8	74.0	9172	2	AAT68748	Aat68748	ATM mutan	c 461	14.8	74.0	96389	9	ADA02675	Ada02675	Mouse Top
389	14.8	74.0	9172	2	AAT68732	Aat68732	ATM mutan	c 462	14.8	74.0	96389	10	ADB72413	Adb72413	Mouse Top
390	14.8	74.0	9180	2	AAT68779	Aat68779	ATM mutan	c 463	14.8	74.0	96389	10	ADB72413	Adb72413	Mouse Top
391	14.8	74.0	9385	2	AAT72683	Aat72683	Cell cycl	c 464	14.8	74.0	96596	10	AD95968	Ad95968	Human NFA
392	14.8	74.0	9385	2	AAX00723	Aax00723	Ataxia-te	c 465	14.8	74.0	96597	9	ADA02720	Ada02720	Human NFA
393	14.8	74.0	9385	2	AAX04532	Aax04532	DNA encod	c 466	14.8	74.0	96597	10	ADB72458	Adb72458	Human NFA
394	14.8	74.0	9385	4	AAT60101	Aat60101	Human ATM	c 467	14.8	74.0	97415	13	ABD33254	Abd33254	Murine ca
395	14.8	74.0	9385	8	ACC49399	Acc49399	Human ATM	c 468	14.8	74.0	100554	11	ACN44624	Acn44624	Murine ca
396	14.8	74.0	9886	12	ADP19628	Adp19628	Human PRO	c 469	14.8	74.0	108566	13	ABD32933	Abd32933	Mouse can
397	14.8	74.0	9886	13	ADP54929	Adp54929	Human PRO	c 470	14.8	74.0	108566	13	ABD32933	Abd32933	Mouse can
398	14.8	74.0	10948	10	ADP87262	Adp87262	Human GPC	c 471	14.8	74.0	109147	12	ADQ97718	Adq97718	Mouse can
399	14.8	74.0	12778	2	AAT68784	Aat68784	ATM mutan	c 472	14.8	74.0	110000	13	ABD32923	Abd32923	Continuation (5 of
400	14.8	74.0	13088	5	AAS69801	Aas69801	DNA encod	c 473	14.8	74.0	110000	13	ABD32923	Abd32923	Continuation (6 of
c 401	14.8	74.0	17286	12	ADH11556	Adh11556	Human bon	c 474	14.8	74.0	114615	11	ACN44298	Acn44298	Human gen
c 402	14.8	74.0	17286	12	ADQ19526	Adq19526	Human sof	c 475	14.8	74.0	114633	11	ACN44332	Acn44332	Mouse gen
c 403	14.8	74.0	21898	9	ADA03041	Ada03041	Mouse mCG	c 476	14.8	74.0	115223	13	ABD33568	Abd33568	Murine ca
c 404	14.8	74.0	21898	9	ADA66325	Ada66325	Mouse mCG	c 477	14.8	74.0	123920	11	ACN44816	Acn44816	Murine ca
c 405	14.8	74.0	21898	10	ADB72779	Adb72779	Mouse mCG	c 478	14.8	74.0	127678	13	ABD32815	Abd32815	Mouse gen
c 406	14.8	74.0	21898	11	ADL27119	Adl27119	Mouse gen	c 479	14.8	74.0	128139	6	AAI64291	Aai64291	RRV genom
c 407	14.8	74.0	25543	11	ACN44384	Acn44384	Mouse gen	c 480	14.8	74.0	133719	3	AAC64754	Aac64754	Macaca mu
c 408	14.8	74.0	26345	11	ACN44384	Acn44384	Mouse gen	c 481	14.8	74.0	137454	12	ADQ97388	Adq97388	Human tum
c 409	14.8	74.0	26345	11	ACN44384	Acn44384	Mouse gen	c 482	14.8	74.0	138941	8	ACC79695	Acc79695	Human tum
c 410	14.8	74.0	28198	10	ADG37080	Adg37080	Mouse pla	c 483	14.8	74.0	140152	12	ADP03002	Adp03002	Human hou
c 411	14.8	74.0	30310	6	AAI38253	Aai38253	Genomic D	c 484	14.8	74.0	140152	12	ADP03002	Adp03002	Human hou
c 412	14.8	74.0	30654	11	ACN45204	Acn45204	Mouse gen	c 485	14.8	74.0	148497	13	ADS88500	Ads88500	Human sof
c 413	14.8	74.0	34637	10	ADP64732	Adp64732	Mouse car	c 486	14.8	74.0	150351	13	ABD33360	Abd33360	Murine ca
c 414	14.8	74.0	35425	12	ADP59455	Adp59455	Human can	c 487	14.8	74.0	150351	13	ABD33360	Abd33360	Murine ca
c 415	14.8	74.0	36047	10	ADP59586	Adp59586	Mouse Nfk	c 488	14.8	74.0	154504	12	ADQ59431	Adq59431	Human can
c 416	14.8	74.0	36048	9	ADA02621	Ada02621	Mouse Nfk	c 489	14.8	74.0	159434	12	ADQ97730	Adq97730	Mouse can
c 417	14.8	74.0	36048	9	ADP72359	Adp72359	Mouse Nfk	c 490	14.8	74.0	167739	9	ADQ58258	Adq58258	Murine tu
c 418	14.8	74.0	37135	9	ADA02645	Ada02645	Mouse Tbx	c 491	14.8	74.0	171936	6	ABE56565	Abes56565	Human SUL
c 419	14.8	74.0	37135	10	ADP72383	Adp72383	Mouse Tbx	c 492	14.8	74.0	171936	12	ADN16205	Adn16205	Human eul
c 420	14.8	74.0	37135	10	ADP59589	Adp59589	Mouse Tbx	c 493	14.8	74.0	182328	12	ADL08128	Adl08128	Human gen
c 421	14.8	74.0	39700	12	ADQ97170	Adq97170	Mouse can	c 494	14.8	74.0	211257	11	ACN44200	Acn44200	Mouse gen
c 422	14.8	74.0	39924	11	ACN45176	Acn45176	Mouse gen	c 495	14.8	74.0	215126	12	ADQ97362	Adq97362	Mouse can
c 423	14.8	74.0	40116	8	ABZ26080	Abz26080	Mouse Dna	c 496	14.8	74.0	215248	12	ADQ97284	Adq97284	Mouse can
c 424	14.8	74.0	41522	11	ACN45008	Acn45008	Mouse gen	c 497	14.8	74.0	235070	11	ACN45174	Acn45174	Human gen
c 425	14.8	74.0	42179	11	ACN45160	Acn45160	Mouse gen	c 498	14.8	74.0	254366	8	ABZ23704	Abz23704	Human pho
c 426	14.8	74.0	42339	11	ACN44508	Acn44508	Mouse gen	c 499	14.8	74.0	254366	8	ABZ23704	Abz23704	Human pho
c 427	14.8	74.0	42881	5	AAF97868	Aaf97868	Human neu	c 500	14.8	74.0	296405	11	ACN44538	Acn44538	Human gen
c 428	14.8	74.0	44990	9	ADA02711	Ada02711	Mouse Vda								
c 429	14.8	74.0	44990	10	ADB72449	Adb72449	Mouse Vda								
c 430	14.8	74.0	44990	10	ADB72449	Adb72449	Mouse Vda								
c 431	14.8	74.0	45315	13	ABD33576	Abd33576	Murine ca								
c 432	14.8	74.0	46137	13	ABD33297	Abd33297	Murine ca								
c 433	14.8	74.0	48643	11	ACN43530	Acn43530	Murine ca								
c 434	14.8	74.0	49502	11	ACN44580	Acn44580	Mouse gen								
c 435	14.8	74.0	52312	13	ABD33555	Abd33555	Murine ca								
c 436	14.8	74.0	52637	13	ADP67083	Adp67083	Mouse can								
c 437	14.8	74.0	54810	13	ABD32759	Abd32759	Mouse can								
c 438	14.8	74.0	61457	10	ADC85383	Adc85383	Mouse Mcm								
c 439	14.8	74.0	62278	13	ABD33618	Abd33618	Murine ca								
c 440	14.8	74.0	65787	9	ADA02603	Ada02603	Mouse Il2								
c 441	14.8	74.0	65787	10	ADB72341	Adb72341	Mouse Il2								
c 442	14.8	74.0	65787	10	ADB72341	Adb72341	Mouse Il2								
c 443	14.8	74.0	66681	13	ADA02903	Ada02903	Mouse Mcm								
c 444	14.8	74.0	67191	9	ADP72641	Adp72641	Murine Mcm								
c 445	14.8	74.0	67191	10	ADP72641	Adp72641	Murine Mcm								
c 446	14.8	74.0	67191	11	ADL95495	Adl95495	Murine MC								
c 447	14.8	74.0	67191	12	ADM74498	Adm74498	Murine ca								
c 448	14.8	74.0	68210	9	ADA66349	Ada66349	Mouse Ppp								
c 449	14.8	74.0	68233	9	ADA03065	Ada03065	Mouse Ppp								
c 450	14.8	74.0	68233	10	ADB72803	Adb72803	Mouse Ppp								
c 451	14.8	74.0	68233	11	ADL27143	Adl27143	Mouse gen								
c 452	14.8	74.0	77287	9	AAD58261	Aad58261	Murine tu								
c 453	14.8	74.0	80423	13	ABD32576	Abd32576	Mouse can								
c 454	14.8	74.0	84830	12	ADL81732	Adl81732	P. aerugi								
c 455	14.8	74.0	87415	11	ACN44948	Acn44948	Mouse gen								
c 456	14.8	74.0	87464	11	ACN44788	Acn44788	Mouse gen								
c 457	14.8	74.0	88607	12	ADQ97648	Adq97648	Mouse can								
c 458	14.8	74.0	90043	11	ACN44608	Acn44608	Mouse gen								

ALIGNMENTS

RESULT 1

ADL13691/c

ID ADL13691 standard; DNA; 1737 BP.

XX

AC ADL13691;

XX

DT 06-MAY-2004 (first entry)

XX

DE Osteoarthritis-associated polymorphic nucleotide #223.

XX

KW ds; gene; osteopathic; antiinflammatory; antiarthritic; gene therapy;

KW joint space narrowing; osteophyte development; joint pain;

KW osteoarthritis; SNP; single nucleotide polymorphism.

XX

OS Homo sapiens.

XX

PN WO2003054166-A2.

XX

PD 03-JUL-2003.

XX

PF 19-DEC-2002; 2002WO-US041225.

XX

PR 20-DEC-2001; 2001US-0342603P.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

Abd32651 Mouse can
Abd32651 Mouse can
Ada02675 Mouse Top
Adb72413 Mouse Top
Ad95923 Mouse Top
Ad95968 Human NFA
Ada02720 Human NFA
Adb72458 Human NFA
Abd33254 Murine ca
Acn44624 Mouse gen
Abd32933 Mouse can
Adq97718 Mouse can
Continuation (2 of
Continuation (5 of
Continuation (6 of
Acn44298 Human gen
Acn44332 Mouse gen
Abd33568 Murine ca
Acn44816 Murine ca
Abd32815 Mouse can
Aai64291 RRV genom
Aac64754 Macaca mu
Acc79695 Human tum
Adp03002 Human hou
Ads88500 Human hou
Adg18925 Human sof
Abd33360 Murine ca
Adq97260 Mouse can
Adq59431 Human can
Adq97730 Mouse can
Aad58258 Murine tu
Abes56565 Human SUL
Adn16205 Mouse eul
Adl08128 Human gen
Acn44200 Mouse gen
Adq97362 Mouse can
Adg97284 Mouse can
Acn45174 Human gen
Abz23704 Human pho
Acn44538 Human gen
Abd32533 Mouse can

ds; gene; osteopathic; antiinflammatory; antiarthritic; gene therapy;
joint space narrowing; osteophyte development; joint pain;
osteoarthritis; SNP; single nucleotide polymorphism.

WO2003054166-A2.

03-JUL-2003.

19-DEC-2002; 2002WO-US041225.

20-DEC-2001; 2001US-0342603P.

(INCY-) INCYTE GENOMICS INC.

PI Jones KA, Schafer A;
 XX WPI; 2003-559141/52.
 XX
 XX Determining susceptibility of an individual to joint space narrowing,
 PT osteophyte development and/or joint pain comprises identifying whether
 PT the individual has at least one polymorphism in a polynucleotide encoding
 PT a protein.
 XX
 XX Disclosure; SEQ ID NO 223; 297pp; English.
 XX
 XX The invention relates to a method of determining susceptibility of an
 CC individual to joint space narrowing and/or osteophyte development and/or
 CC joint pain comprising identifying whether the individual has at least one
 CC polymorphism in a polynucleotide encoding at least one of the protein
 CC listed in the specification. The methods, composition and agent are
 CC useful for modulating the susceptibility of an individual to joint space
 CC narrowing and/or osteophyte development and/or joint pain that is
 CC associated with a disease, preferably osteoarthritis. The cell line and
 CC the non-human animal are useful for screening for an agent for diagnosing
 CC an individual having susceptibility to joint space narrowing and/or
 CC osteophyte development and/or joint pain. This sequence corresponds to
 CC the polynucleotide encoding a protein listed in the specification. (Note:
 CC the sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences).
 XX
 XX Sequence 1737 BP; 232 A; 571 C; 603 G; 331 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 20; DB 10; Length 1737;
 Best Local Similarity 100.0%; Pred. No. 4.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGGGCGTCTCTGAGTAGCAG 20
 DB 1099 AGGGCGTCTCTGAGTAGCAG 1080
 RESULT 2
 ADL13692/c
 ID ADL13692 standard; DNA; 1737 BP.
 XX
 XX ADL13692;
 XX
 XX 06-MAY-2004 (first entry)
 XX
 XX Osteoarthritis-associated polymorphic nucleotide #224.
 XX
 XX ds; gene; osteopathic; antiinflammatory; antiarthritic; gene therapy;
 KW joint space narrowing; osteophyte development; joint pain;
 KW osteoarthritis; SNP; single nucleotide polymorphism.
 XX
 XX Homo sapiens.
 OS
 XX WO2003054166-A2.
 PN
 XX 03-JUL-2003.
 PD
 XX 19-DEC-2002; 2002WO-US041225.
 PF
 XX 20-DEC-2001; 2001US-0342603P.
 PR
 XX (INCY-) INCYTE GENOMICS INC.
 PA
 XX Jones KA, Schafer A;
 PI
 XX WPI; 2003-559141/52.
 XX
 XX Determining susceptibility of an individual to joint space narrowing,
 PT osteophyte development and/or joint pain comprises identifying whether
 PT the individual has at least one polymorphism in a polynucleotide encoding
 PT a protein.
 XX

PS Disclosure; SEQ ID NO 224; 297pp; English.
 XX
 XX The invention relates to a method of determining susceptibility of an
 CC individual to joint space narrowing and/or osteophyte development and/or
 CC joint pain comprising identifying whether the individual has at least one
 CC polymorphism in a polynucleotide encoding at least one of the protein
 CC listed in the specification. The methods, composition and agent are
 CC useful for modulating the susceptibility of an individual to joint space
 CC narrowing and/or osteophyte development and/or joint pain that is
 CC associated with a disease, preferably osteoarthritis. The cell line and
 CC the non-human animal are useful for screening for an agent for diagnosing
 CC an individual having susceptibility to joint space narrowing and/or
 CC osteophyte development and/or joint pain. This sequence corresponds to
 CC the polynucleotide encoding a protein listed in the specification. (Note:
 CC the sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences).
 XX
 XX Sequence 1737 BP; 232 A; 569 C; 604 G; 332 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 20; DB 10; Length 1737;
 Best Local Similarity 100.0%; Pred. No. 4.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGGGCGTCTCTGAGTAGCAG 20
 DB 1099 AGGGCGTCTCTGAGTAGCAG 1080
 RESULT 3
 ADL13694/c
 ID ADL13694 standard; DNA; 2087 BP.
 XX
 XX ADL13694;
 XX
 XX 06-MAY-2004 (first entry)
 XX
 XX Osteoarthritis-associated polymorphic nucleotide #226.
 XX
 XX ds; gene; osteopathic; antiinflammatory; antiarthritic; gene therapy;
 KW joint space narrowing; osteophyte development; joint pain;
 KW osteoarthritis; SNP; single nucleotide polymorphism.
 XX
 XX Homo sapiens.
 OS
 XX WO2003054166-A2.
 PN
 XX 03-JUL-2003.
 PD
 XX 19-DEC-2002; 2002WO-US041225.
 PF
 XX 20-DEC-2001; 2001US-0342603P.
 PR
 XX (INCY-) INCYTE GENOMICS INC.
 PA
 XX Jones KA, Schafer A;
 PI
 XX WPI; 2003-559141/52.
 XX
 XX Determining susceptibility of an individual to joint space narrowing,
 PT osteophyte development and/or joint pain comprises identifying whether
 PT the individual has at least one polymorphism in a polynucleotide encoding
 PT a protein.
 XX
 XX Disclosure; SEQ ID NO 226; 297pp; English.
 XX
 XX The invention relates to a method of determining susceptibility of an
 CC individual to joint space narrowing and/or osteophyte development and/or
 CC joint pain comprising identifying whether the individual has at least one
 CC polymorphism in a polynucleotide encoding at least one of the protein
 CC listed in the specification. The methods, composition and agent are
 CC useful for modulating the susceptibility of an individual to joint space
 CC narrowing and/or osteophyte development and/or joint pain that is

CC associated with a disease, preferably osteoarthritis. The cell line and
CC the non-human animal are useful for screening for an agent for diagnosing
CC an individual having susceptibility to joint space narrowing and/or
CC osteophyte development and/or joint pain. This sequence corresponds to
CC the polynucleotide encoding a protein listed in the specification. (Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences).

XX SQ Sequence 2087 BP; 302 A; 650 C; 712 G; 423 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 2087;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
Db 1134 AGGGCGTCTCTGAGTAGCAG 1115

RESULT 4
ADL13690/c
ID ADL13690 standard; DNA; 2088 BP.

XX AC ADL13690;

XX DT 06-MAY-2004 (first entry)

XX DE Osteoarthritis-associated polymorphic nucleotide #222.

XX ds; gene; osteopathic; antiinflammatory; antiarthritic; gene therapy;

XX joint space narrowing; osteophyte development; joint pain;

XX osteoarthritis; SNP; single nucleotide polymorphism.

XX OS Homo sapiens.

XX PN WO2003054166-A2.

XX PD 03-JUL-2003.

XX PF 19-DEC-2002; 2002WO-US041225.

XX PR 20-DEC-2001; 2001US-0342603P.

XX PA (INCY-) INCYTE GENOMICS INC.

XX PI Jones KA, Schafer A;

XX WPI; 2003-559141/52.

XX Determining susceptibility of an individual to joint space narrowing,
PT osteophyte development and/or joint pain comprises identifying whether
PT the individual has at least one polymorphism in a polynucleotide encoding
PT a protein.

PS Disclosure; SEQ ID NO 222; 297pp; English.

XX The invention relates to a method of determining susceptibility of an
CC individual to joint space narrowing and/or osteophyte development and/or
CC joint pain comprising identifying whether the individual has at least one
CC polymorphism in a polynucleotide encoding at least one of the protein
CC listed in the specification. The methods, composition and agent are
CC useful for modulating the susceptibility of an individual to joint space
CC narrowing and/or osteophyte development and/or joint pain that is
CC associated with a disease, preferably osteoarthritis. The cell line and
CC the non-human animal are useful for screening for an agent for diagnosing
CC an individual having susceptibility to joint space narrowing and/or
CC osteophyte development and/or joint pain. This sequence corresponds to
CC the polynucleotide encoding a protein listed in the specification. (Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences).

SQ Sequence 2088 BP; 302 A; 652 C; 711 G; 423 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 2088;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
Db 1134 AGGGCGTCTCTGAGTAGCAG 1115

RESULT 5
AAT99541/c

ID AAT99541 standard; cDNA; 2116 BP.

XX AC AAT99541;

XX DT 21-MAY-1998 (first entry)

XX DE Human hyaluronan synthase cDNA clone 30C.

XX KW Hyaluronan synthase; HAS gene; human; hyaluronic acid; cell adhesion;
XX wound healing; vulnery; tissue repair; scar; keloid; therapy; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 36..1172

XX FT polyA_signal /*tag= a

XX FT 2066..2071 /*tag= b

XX PN WO9740174-A1.

XX PD 30-OCT-1997.

XX PF 17-APR-1997; 97WO-US006350.

XX PR 22-APR-1996; 96US-00635552.

XX PA (LEUK-) LEUKOSITE INC.

XX PI Briskin MJ;

XX WPI; 1997-549359/50.

XX P-PSDB; AAW26765.

XX Human hyaluronan synthase - useful for recombinant production of
PT hyaluronic acid for wound healing, tissue repair and reducing
PT hypertrophic scar and keloid formation.

PS Claim 3; Page 36-38; 58pp; English.

XX cDNA clone 30C includes a coding region for hyaluronan synthase (HAS)
CC (see AAW26765), an enzyme involved in the synthesis of hyaluronan
CC (hyaluronic acid) and which has the ability to confer cell adhesion by
CC the lymphocyte receptor CD44. Clone 30C was isolated using an expression
CC cloning system developed to isolate cDNA clones that encode proteins that
CC confer adhesion of the murine T cell lymphoma TK1. A human mesenteric
CC lymph node expression library was constructed that, upon transfection
CC into CHO/P cells, yielded clone 30C that mediated rosetting of TK1 cells
CC to some of the transfectants. The isolated clone can be utilised in a
CC claimed method for producing HAS in host cells. Such host cells are used
CC in a claimed method for the production of hyaluronan. Hyaluronan is
CC useful for wound healing and tissue repair, and can reduce or prevent
CC hypertrophic scars and keloid formation. It is also used in eye surgery
CC as a replacement for vitreous fluid

XX SQ Sequence 2116 BP; 330 A; 651 C; 712 G; 423 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 2116;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 AGGGCGTCTCTGAGTAGCAG 20
Db 1134 AGGGCGTCTCTGAGTAGCAG 1115

RESULT 6
AAT96713/c
ID AAT96713 standard; DNA; 2117 BP.
XX
AC AAT96713;
XX
XX
DT 22-APR-1998 (first entry)
DE
DE Human hyaluronate synthetase coding sequence.
XX
XX Hyaluronate synthetase; human; hyaluronic acid; drug preparation;
KW cosmetic preparation; gene therapy; carcinogenesis; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 149..1780
FT /*tag= a
XX
XX WO9738113-A1.
XX
XX 16-OCT-1997.
XX
XX 31-MAR-1997; 97WO-JP001111.
XX
XX 05-APR-1996; 96JP-00084326.
XX 30-APR-1996; 96JP-00109663.
XX
XX (SEKG ) SEIKAGAKU CORP.
XX
XX Itano N, Kimata K;
XX
XX WPI; 1997-512726/47.
XX P-PSDB; AAW36503.
XX
XX DNA encoding human hyaluronate synthetase - for industrial scale
PT production of hyaluronic acid used in generating anti-carcinogenic drugs
PT or for cosmetics.
XX
XX Claim 3; Page 23-27; 35pp; Japanese.
XX
XX This sequence encodes a human hyaluronate synthetase, and is the coding
CC sequence of the invention. The encoded enzyme is useful for industrial
CC scale production of hyaluronic acid for use in the preparation of drugs
CC and cosmetics. The drugs can also be used in compositions for the
CC treatment of disorders involving the lowering of hyaluronic acid
CC production. The peptides may be used for the preparation of antibodies
CC recognising hyaluronate synthetase, e.g. for diagnostic purposes.
CC Antisense DNA or RNA corresponding to the DNA can be used in gene therapy
CC treatment of carcinogenesis
XX
XX Sequence 2117 BP; 306 A; 673 C; 703 G; 435 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 20; DB 2; Length 2117;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
Db 1142 AGGGCGTCTCTGAGTAGCAG 1123

RESULT 7
ADL13693
ID ADL13693 standard; DNA; 231222 BP.
XX
XX ADL13693;
AC

QY 1 AGGGCGTCTCTGAGTAGCAG 20
Db 143286 AGGGCGTCTCTGAGTAGCAG 143305

Query Match 100.0%; Score 20; DB 10; Length 231222;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
Db 143286 AGGGCGTCTCTGAGTAGCAG 143305

RESULT 8
ABZ76734/c
ID ABZ76734 standard; cDNA; 1752 BP.
XX
XX ABZ76734;
AC
XX
XX 01-APR-2000; (first entry)
DT
XX
DE Mouse hyaluronan synthase 1 encoding cDNA SEQ ID NO:1.
XX
XX Mouse; hyaluronan synthase; HAS; HAS1; enzyme; ophthalmological;
KW osteopathic; antiarthritic; gene therapy; angiogenesis inhibitor;
KW hyaluronic acid; dihydrazide; bioconjugate; dry eye syndrome; eye;
KW osteoarthritis; gene; ss.

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XX
DT 06-MAY-2004 (first entry)
DE
DE Osteoarthritis-associated polymorphic nucleotide #225.
XX
KW ds; gene; osteopathic; antiinflammatory; antiarthritic; gene therapy;
KW joint space narrowing; osteophyte development; joint pain;
KW osteoarthritis; SNP; single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
XX WO2003054166-A2.
XX
XX 03-JUL-2003.
XX
XX 19-DEC-2002; 2002WO-US041225.
XX
XX 20-DEC-2001; 2001US-0342603P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Jones KA, Schafer A;
XX WPI; 2003-559141/52.
XX
XX Determining susceptibility of an individual to joint space narrowing,
XX osteophyte development and/or joint pain comprises identifying whether
XX the individual has at least one polymorphism in a polynucleotide encoding
XX a protein.
XX
XX Disclosure; SEQ ID NO 225; 297pp; English.
XX
XX The invention relates to a method of determining susceptibility of an
XX individual to joint space narrowing and/or osteophyte development and/or
XX joint pain comprising identifying whether the individual has at least one
XX polymorphism in a polynucleotide encoding at least one of the protein
XX listed in the specification. The methods, composition and agent are
XX useful for modulating the susceptibility of an individual to joint space
XX narrowing and/or osteophyte development and/or joint pain that is
XX associated with a disease, preferably osteoarthritis. The cell line and
XX the non-human animal are useful for screening for an agent for diagnosing
XX an individual having susceptibility to joint space narrowing and/or
XX osteophyte development and/or joint pain. This sequence corresponds to
XX the polynucleotide encoding a protein listed in the specification. (Note:
XX The sequence data for this patent did not form part of the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences).
XX
XX Sequence 231222 BP; 64006 A; 52087 C; 53478 G; 61650 T; 0 U; 1 Other;
SQ

Query Match 100.0%; Score 20; DB 10; Length 231222;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
Db 143286 AGGGCGTCTCTGAGTAGCAG 143305

RESULT 8
ABZ76734/c
ID ABZ76734 standard; cDNA; 1752 BP.
XX
XX ABZ76734;
AC
XX
XX 01-APR-2000; (first entry)
DT
XX
DE Mouse hyaluronan synthase 1 encoding cDNA SEQ ID NO:1.
XX
XX Mouse; hyaluronan synthase; HAS; HAS1; enzyme; ophthalmological;
KW osteopathic; antiarthritic; gene therapy; angiogenesis inhibitor;
KW hyaluronic acid; dihydrazide; bioconjugate; dry eye syndrome; eye;
KW osteoarthritis; gene; ss.

```

```

XX OS Mus sp.
XX FH Key Location/Qualifiers
XX FT CDS 1..1752
XX FT /*tag= a
XX FT /product= "hyaluronan synthase 1 (HAS1)"
XX PN WO2003006068-A1.
XX XX
XX PD 23-JAN-2003.
XX PF 10-JUL-2001; 2001WO-US021785.
XX XX
XX PR 10-JUL-2001; 2001WO-US021785.
XX XX
XX PA (CLEA-) CLEAR SOLUTIONS BIOTECH INC.
XX XX
XX PI Dehazya P, Chen W;
XX XX
XX DR WPI; 2003-221664/21.
XX DR P-PSDB; ABP96028.
XX XX
XX PT Novel dihydrazide derivatized hyaluronic acid/nucleic acid bioconjugate
XX PT for treating dry eye syndrome, has derivatized hyaluronic acid
XX PT crosslinked to nucleic acid encoding protein with hyaluronan synthase
XX PT activity.
XX XX
XX PS Claim 19; Page 56; 62pp; English.
XX XX
XX CC The present invention describes a dihydrazide derivatised hyaluronic acid
XX CC (HA)/nucleic acid (NA) bioconjugate (I), with derivatised HA linked to NA
XX CC encoding protein with hyaluronan synthase (HAS) activity, where NA has
XX CC sequence with 79-85% sequence identity (SI) to a sequence of 1752, 1659
XX CC or 1665 nucleotides (see ABZ76734 to ABZ76736) or a sequence encoding
XX CC proteins with 66-90% SI to a sequence of 583, 552 or 554 amino acids (see
XX CC ABP96028 to ABP96030). (I) has ophthalmological, osteopathic and
XX CC antiarthritic activities, and can be used in gene therapy and as an
XX CC inhibitor of angiogenesis, and as an inducer of expression of (HA) in
XX CC human corneal epithelial cell. (I) is useful for transfecting a cell of
XX CC an eye with nucleic acid, where the nucleic acid comprises (ABZ76734 to
XX CC ABZ76736), by contacting the cell with (I) comprising the nucleic acid.
XX CC (I) is useful for treating dry eye syndrome in an individual. (I) is
XX CC useful in gene therapy applications for the treatment of a variety of
XX CC medical conditions including dry eye syndrome or other medical conditions
XX CC where an increase in the production of (HA) in the eye would be
XX CC therapeutic (e.g., osteoarthritis of the articular joints). (I) is also
XX CC useful for inhibiting angiogenesis for the treatment of macular
XX CC degeneration or genes related to lipid biosynthesis that helps to restore
XX CC the lipid component of the tear film, and as reagents for in vitro
XX CC transfection of any cell, preferably a eukaryotic cell, more preferably
XX CC a human eye cell. The present sequence encodes mouse HAS1 which is used
XX CC in the exemplification of the present invention
XX XX
XX SQ Sequence 1752 BP; 308 A; 505 C; 548 G; 391 T; 0 U; 0 Other;
XX XX
XX Query Match 87.0%; Score 17.4; DB 8; Length 1752;
XX Best Local Similarity 94.7%; Pred. No. 91;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX XX
XX QY 1 AGGGCGTCTCTGAGTAGCA 19
XX |||||||
XX Db 1114 AGGGCGTCTCCGAGTAGCA 1096
XX XX
XX RESULT 9
XX AAD59442/C
XX ID AAD59442 standard; DNA; 1752 BP.
XX XX
XX AC AAD59442;
XX XX
XX DT 18-DEC-2003 (first entry)
XX XX
XX XX

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DE Mouse hyaluronan synthase (HAS) 1 DNA.
XX XX
XX KW Mouse; hyaluronic acid; HA; hyaluronan synthase; HAS; dry eye syndrome;
XX KW eye cell; osteoarthritis; gene therapy; gene; ds.
XX OS Mus sp.
XX FH Key Location/Qualifiers
XX FT CDS 1..1752
XX FT /*tag= a
XX FT /product= "Mouse hyaluronan synthase 1"
XX PN US2003087850-A1.
XX XX
XX PD 08-MAY-2003.
XX PF 10-JUL-2001; 2001US-00902939.
XX XX
XX PR 10-JUL-2001; 2001US-00902939.
XX XX
XX PA (DEHA/) DEHAZYA P.
XX PA (CHEN/) CHEN W.
XX XX
XX PI Dehazya P, Chen W;
XX XX
XX DR WPI; 2003-755151/71.
XX DR P-PSDB; AAE39152.
XX XX
XX PT Dihydrazide derivatized hyaluronic acid/nucleic acid bioconjugate
XX PT comprising derivatized hyaluronic acid cross linked to nucleic acid
XX PT encoding hyaluronan synthase useful for treating dry eye syndrome.
XX XX
XX PS Claim 1; Page 12-13; 31pp; English.
XX XX
XX CC The invention relates to dihydrazide derivatised hyaluronic acid (HA)/
XX CC nucleic acid bioconjugate comprising derivatised HA cross linked to
XX CC nucleic acid encoding hyaluronan synthase (HAS). The invention is useful
XX CC for transfecting an eye cell of an individual. It is useful for treating
XX CC dry eye syndrome and osteoarthritis of the particular joints. The
XX CC invention is also useful in gene therapy. The present sequence is mouse
XX CC HAS1 DNA
XX XX
XX SQ Sequence 1752 BP; 308 A; 505 C; 548 G; 391 T; 0 U; 0 Other;
XX XX
XX Query Match 87.0%; Score 17.4; DB 10; Length 1752;
XX Best Local Similarity 94.7%; Pred. No. 91;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX XX
XX QY 1 AGGGCGTCTCTGAGTAGCA 19
XX |||||||
XX Db 1114 AGGGCGTCTCCGAGTAGCA 1096
XX XX
XX RESULT 10
XX AAT91655/C
XX ID AAT91655 standard; DNA; 2102 BP.
XX XX
XX AC AAT91655;
XX XX
XX DT 17-OCT-2003 (revised)
XX DT 19-DEC-1997 (first entry)
XX XX
XX DE Mouse hyaluronate synthase genomic DNA.
XX XX
XX KW Hyaluronate synthase; hyaluronic acid; polysaccharide; ds.
XX XX
XX OS Mus sp; (strain FM3A).
XX XX
XX FH Key Location/Qualifiers
XX FT CDS 49..1800
XX FT /*tag= a
XX FT /product= "Hyaluronate synthase"
XX XX

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PN JP09224674-A.
 XX
 PD
 XX
 PF 26-FEB-1996; 96JP-00038336.
 XX
 PR 26-FEB-1996; 96JP-00038336.
 XX
 PA (KAGG) KAGAKU GIJUTSUCHO CHOKAN KANBO.
 XX
 DR WPI: 1997-484102/45.
 DR P-PSDB; AA030704.
 XX
 PT Hyaluronate synthase isolated from mouse cells - useful for large-scale
 PT production of hyaluronic acid.
 XX
 PS Claim 2; Page 10-13; 15pp; Japanese.
 XX
 CC A mouse-derived cell strain, FM3A P15-A, was cultured in Eagle minimal
 CC medium containing 10 % heat-inactivated bovine serum, twice concentration
 CC of amino acids and vitamins and penicillin and streptomycin at 37 degrees
 CC Celsius. The culture was subjected to immobilised erythrocyte exclusion
 CC to examine the extent of extracellular formation of hyaluronic acid
 CC matrix. Cells which showed high formation were recovered and named FM3A
 CC HAI. Cells synthesising no hyaluronic acid were recovered and named HAS-
 CC (HAS- P cell). Poly(A) + RNA was isolated from FM3A HAI and cDNA was
 CC prepared and was used for constructing a library in HAS- P cells. Cells
 CC having hyaluronic acid synthetic activity were selected from the
 CC transformants and plasmid DNA was recovered and amplified in E.coli. The
 CC resulting genomic DNA sequence codes for hyaluronate synthase having a
 CC sequence of 583 amino acids which is used for large-scale production of
 CC hyaluronic acid, a component of drugs and cosmetics. (Updated on 17-OCT-
 CC 2003 to standardise OS field)
 XX
 SQ Sequence 2102 BP; 399 A; 565 C; 640 G; 498 T; 0 U; 0 Other;
 Query Match 87.0%; Score 17.4; DB 2; Length 2102;
 Best Local Similarity 94.7%; Pred. No. 92;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AGGGCGTCTCTGAGTAGCA 19
 Db 1162 AGGGCGTCTCCGAGTAGCA 1144
 RESULT 11
 AAZ10862/c
 ID AAZ10862 standard; DNA; 2102 BP.
 AC
 AC AAZ10862;
 XX
 DT 19-OCT-1999 (first entry)
 DE Hyaluronate synthase coding sequence.
 XX
 KW Hyaluronate synthase; promoter; mouse; cell growth inhibitor; ds.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 49..1800
 FT /*tag= a
 FT /product= "HAS1"
 FT /note= "modified hyaluronate synthase protein"
 XX
 PN JP2000004886-A.
 PD 11-JAN-2000.
 XX
 PF 24-JUN-1998; 98JP-00193788.
 XX
 PR 24-JUN-1998; 98JP-00193788.
 XX
 PA (SEKK) SEIKAGAKU KOGYO CO LTD.
 XX
 DR WPI: 2000-140125/13.
 DR P-PSDB; AAY68491.
 XX
 PT A hyaluronate synthase modified protein - useful as a research reagent
 PT for biochemical research and medical development.
 XX
 PS Claim 18; Page 12-14; 30pp; Japanese.
 XX
 CC The present invention describes a recombinant protein which consists of
 CC three continuous regions (N-terminal region, internal region and C-
 CC terminal region) where one or two regions among the above three regions
 CC is selected from the three hyaluronate synthase (HAS) modified proteins
 CC HAS1, HAS2 and HAS3 (e.g. a protein made from HAS1 amino acids 1 to 71,
 CC HAS2 amino acids 52 to 379 and HAS1 amino acids 410 to 583). The protein
 CC is useful as a research reagent for biochemical research and medical
 CC development. The invention provides a HAS modified protein of increased
 CC or lowered activity. The present sequence encodes mouse HAS1

XX
 DR WPI: 1999-496653/42.
 DR P-PSDB; AAY32503.
 XX
 PT New promoter DNA of hyaluronate synthase - used to specifically express
 PT gene with cell growth inhibiting activity.
 XX
 PS Example 1; Page 8-10; 13pp; Japanese.
 XX
 CC This sequence represents the mouse hyaluronate synthase coding sequence,
 CC and was used to isolate the hyaluronate synthase promoter of the
 CC invention. The promoter can be used for specifically expressing a gene
 CC having cell growth inhibiting activity
 XX
 SQ Sequence 2102 BP; 399 A; 565 C; 640 G; 498 T; 0 U; 0 Other;
 Query Match 87.0%; Score 17.4; DB 2; Length 2102;
 Best Local Similarity 94.7%; Pred. No. 92;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AGGGCGTCTCTGAGTAGCA 19
 Db 1162 AGGGCGTCTCCGAGTAGCA 1144
 RESULT 12
 AAZ88199/c
 ID AAZ88199 standard; cDNA to mRNA; 2102 BP.
 AC
 AC AAZ88199;
 XX
 DT 27-APR-2000 (first entry)
 DE Mouse hyaluronate synthase modified protein HAS1 encoding cDNA.
 XX
 KW Mouse; murine; hyaluronate synthase; modification; HAS1; HAS2; HAS3;
 KW research reagent; biochemical research; medical development; ds.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 49..1800
 FT /*tag= a
 FT /product= "HAS1"
 FT /note= "modified hyaluronate synthase protein"
 XX
 PN JP2000004886-A.
 PD 11-JAN-2000.
 XX
 PF 24-JUN-1998; 98JP-00193788.
 XX
 PR 24-JUN-1998; 98JP-00193788.
 XX
 PA (SEKK) SEIKAGAKU KOGYO CO LTD.
 XX
 DR WPI: 2000-140125/13.
 DR P-PSDB; AAY68491.
 XX
 PT A hyaluronate synthase modified protein - useful as a research reagent
 PT for biochemical research and medical development.
 XX
 PS Claim 18; Page 12-14; 30pp; Japanese.
 XX
 CC The present invention describes a recombinant protein which consists of
 CC three continuous regions (N-terminal region, internal region and C-
 CC terminal region) where one or two regions among the above three regions
 CC is selected from the three hyaluronate synthase (HAS) modified proteins
 CC HAS1, HAS2 and HAS3 (e.g. a protein made from HAS1 amino acids 1 to 71,
 CC HAS2 amino acids 52 to 379 and HAS1 amino acids 410 to 583). The protein
 CC is useful as a research reagent for biochemical research and medical
 CC development. The invention provides a HAS modified protein of increased
 CC or lowered activity. The present sequence encodes mouse HAS1

```
XX SQ Sequence 2102 BP; 399 A; 565 C; 640 G; 498 T; 0 U; 0 Other;
Query Match 87.0%; Score 17.4; DB 3; Length 2102;
Best Local Similarity 94.7%; Pred. No. 92;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCA 19
DB 1162 AGGGCGTCTCCGAGTAGCA 1144

RESULT 13
AAA39987/c
ID AAA39987 standard; cDNA; 2102 BP.
XX AC
XX AAA39987;
XX DT 19-OCT-2000 (first entry)
XX DE Murine HAS1 cDNA.
XX KW Murine; HAS1; hyaluronate synthase; marker gene; intracellular loop;
XX KW gene targeting; ss.
XX OS Mus sp.
XX FH Key Location/Qualifiers
XX FT CDS 49..1800
XX FT /*tag= a
XX FT /product= "HAS1"
XX PN JP2000116382-A.
XX PD 25-APR-2000.
XX PF 13-OCT-1998; 98JP-00291201.
XX PR 13-OCT-1998; 98JP-00291201.
XX PA (SEKG ) SEIKAGAKU KOGYO CO LTD.
XX WPI; 2000-369404/32.
XX P-PSDB; AAB09948.
XX PT DNA used for gene targeting of the hyaluronate synthase gene (HAS1) .
XX PS Example; Page 7-9; 14pp; Japanese.
XX CC This invention describes a novel DNA which contains an heterologous DNA
CC (i) to be introduced to chromosomal DNA of a host cell, a first and
CC second homologous region DNA (II) connected respectively to the 5' and 3'
CC sides of the introduced DNA, and a negative marker gene (III) expressable
CC in the host cell. (I) contains a positive marker gene expressable in the
CC host cell. (I), (II) and the region encoding the intracellular loop of
CC the hyaluronate synthase (HAS) 1 protein from chromosomal DNA is
CC constituted so as to cause a homologous recombination. The DNA can be
CC used for gene targeting of the HAS1 gene. This sequence encodes the
CC murine HAS1 protein described in the method of the invention
XX SQ Sequence 2102 BP; 399 A; 565 C; 640 G; 498 T; 0 U; 0 Other;
Query Match 87.0%; Score 17.4; DB 3; Length 2102;
Best Local Similarity 94.7%; Pred. No. 92;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCA 19
DB 1162 AGGGCGTCTCCGAGTAGCA 1144

RESULT 14
ACH89039/c
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```
ID ACH89039 standard; DNA; 239 BP.
XX AC
XX ACH89039;
XX DT 29-JUL-2004 (first entry)
XX DE Human genome derived single exon probe #22234.
XX KW Human; probe; ss; gene expression; single exon probe; microarray;
XX KW alternative splicing event; genomic alteration.
XX OS Homo sapiens.
XX PN US2003194704-A1.
XX PD 16-OCT-2003.
XX PF 03-APR-2002; 2002US-00029386.
XX PR 03-APR-2002; 2002US-00029386.
XX PA (PENN/) PENN S G.
XX PA (RANK/) RANK D R.
XX PA (HANZ/) HANZEL D K.
XX PI Penn SG, Rank DR, Hanzel DK;
XX WPI; 2004-119264/12.
XX DR New human genome-derived single exon nucleic acid probes useful for human
XX PT gene expression analysis, for identifying or characterizing alternative
XX PT splicing events, for assessing genomic alterations or as tools for
XX PT surveying tissues.
XX PS Claim 1; SEQ ID NO 22234; 80pp; English.
XX CC The invention relates to a nucleic acid probe for measuring human gene
XX CC expression, comprising any of the 27,400 fully defined nucleotide
XX CC sequences in the specification, or their complements or fragments, and
XX CC encoding at least 8 amino acids of any of the 688 amino acid sequences
XX CC fully defined in the specification. The probe is a single exon probe that
XX CC hybridises under high stringency conditions to a nucleic acid molecule
XX CC expressed in human cells or tissues. Also included are a spatially-
XX CC addressable set of single exon nucleic acid probes for measuring human
XX CC gene expression (comprising a plurality of single exon nucleic acid
XX CC probes cited above, where each of the plurality of probes is separately
XX CC and addressably isolatable or amplifiable from the plurality), a single
XX CC exon microarray for measuring human gene expression, a method of
XX CC measuring human gene expression, a vector comprising the single exon
XX CC probe cited above, an ORF-encoded peptide comprising at least 8
XX CC contiguous amino acids of any of the above- mentioned amino acid
XX CC sequences (optionally with conservative amino acid substitutions), an
XX CC isolated antibody that binds specifically to a peptide cited above,
XX CC methods of selling and/or licensing single exon probes or microarrays to
XX CC a customer desiring to measure gene expression, a method of providing
XX CC human gene expression data by subcription, and a computer-readable
XX CC storage medium which contains a database having a plurality of records
XX CC (each record including data on the expression of a single exon probe
XX CC cited above. The probe, methods and apparatus are useful in gene
XX CC expression analysis. The probes may be used as tools for surveying
XX CC tissues to detect the presence of expressed messages that contain their
XX CC specific exon or in constructing genome-derived single exon microarrays.
XX CC In addition, the probes are used in identifying and characterising
XX CC alternative splicing events, in detecting and characterising gross
XX CC alterations in the genomic locus that includes their exon, in assessing
XX CC smaller genomic alterations, in priming the synthesis of nucleic acids,
XX CC or in expressing the ORF-encoded peptide. The present sequence is a human
XX CC single exon probe of the invention. Note: The sequence data for this
XX CC patent did not form part of the printed specification, but was obtained
XX CC in electronic format directly from USPTO at
XX CC seqdata.uspto.gov/sequence.html?DocId=20030194704
XX SQ Sequence 239 BP; 54 A; 58 C; 59 G; 68 T; 0 U; 0 Other;
```

Query Match 84.0%; Score 16.8; DB 12; Length 239;
 Best Local Similarity 90.0%; Pred. No. 1.5e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
 ||||| ||||| ||||| |||||
 Db 113 AGGGCATCTCTGAGTTGCAG 94

RESULT 15
 AAC10010
 ID AAC10010 standard; cDNA; 278 BP.
 XX
 AC AAC10010;
 XX
 DT 06-OCT-2000 (first entry)
 XX
 DE Human secreted protein 5' EST, SEQ ID NO: 14085.
 XX
 DE Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1033401-A2.
 XX
 PD 06-SEP-2000.
 XX
 PP 21-FEB-2000; 2000EP-00200610.
 XX
 PR 26-FEB-1999; 99US-0122487P.
 XX
 PA (GEST) GENSET.
 XX
 PI Dumas Milne Edwards J, Duclert A, Giordano J;
 WPI; 2000-500381/45.
 DR
 DR
 XX
 XX
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
 XX
 PS Claim 1; SEQ ID NO 14085; 71pp + Sequence Listing; English.
 CC
 CC The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences
 CC derived from the 5' ends of mRNAs and even in those cases where longer
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
 CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used
 CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
 CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC They are used to obtain upstream regulatory sequences and to design
 CC expression and secretion vectors
 XX
 SQ Sequence 278 BP; 74 A; 70 C; 65 G; 69 T; 0 U; 0 Other;

Query Match 84.0%; Score 16.8; DB 3; Length 278;
 Best Local Similarity 90.0%; Pred. No. 1.5e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
 ||||| ||||| ||||| |||||
 Db 113 AGGGCATCTCTGAGTTGCAG 132

RESULT 16
 AAC02292
 ID AAC02292 standard; cDNA; 313 BP.
 XX
 AC AAC02292;
 XX
 DT 06-OCT-2000 (first entry)
 XX
 DE Human secreted protein 5' EST, SEQ ID NO: 2290.
 XX
 DE Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1033401-A2.
 XX
 PD 06-SEP-2000.
 XX
 PP 21-FEB-2000; 2000EP-00200610.
 XX
 PR 26-FEB-1999; 99US-0122487P.
 XX
 PA (GEST) GENSET.
 XX
 PI Dumas Milne Edwards J, Duclert A, Giordano J;
 WPI; 2000-500381/45.
 DR
 DR
 XX
 XX
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
 XX
 PS Claim 1; SEQ ID NO 2290; 71pp + Sequence Listing; English.
 CC
 CC The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. An ORF has been identified within the
 CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
 CC derived from 30 different tissues. EST sequences usually correspond
 CC mainly to the 3' untranslated region (UTR) of the mRNA because they are
 CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
 CC well suited for isolating cDNA sequences derived from the 5' ends of
 CC mRNAs and even in those cases where longer cDNA sequences have been
 CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
 CC mRNAs with intact 5' ends and can therefore be used to obtain full length
 CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
 CC gene therapy and chromosome mapping procedures. They are used to obtain
 CC upstream regulatory sequences and to design expression and secretion
 CC vectors
 XX
 SQ Sequence 313 BP; 83 A; 78 C; 72 G; 76 T; 0 U; 4 Other;

Query Match 84.0%; Score 16.8; DB 3; Length 313;
 Best Local Similarity 90.0%; Pred. No. 1.5e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
 ||||| ||||| ||||| |||||
 Db 113 AGGGCATCTCTGAGTTGCAG 132

RESULT 17
 ACH75339/c
 ID ACH75339 standard; DNA; 595 BP.
 XX
 AC ACH75339;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Human genome derived single exon probe #8534.
 XX
 DE Human; probe; ss; gene expression; single exon probe; microarray;
 KW alternative splicing event; genomic alteration.
 XX

```
OS Homo sapiens.
XX US2003194704-A1.
XX 16-OCT-2003.
XX 03-APR-2002; 2002US-00029386.
XX 03-APR-2002; 2002US-00029386.
XX (PENN/) PENN S G.
XX (RANK/) RANK D R.
XX (HANZ/) HANZEL D K.
XX Penn SG, Rank DR, Hanzel DK;
XX WPI; 2004-119264/12.
XX New human genome-derived single exon nucleic acid probes useful for human
XX gene expression analysis, for identifying or characterizing alternative
XX splicing events, for assessing genomic alterations or as tools for
XX surveying tissues.
XX Claim 15; SEQ ID NO 8534; 80pp; English.
XX The invention relates to a nucleic acid probe for measuring human gene
XX expression, comprising any of the 27,400 fully defined nucleotide
XX sequences in the specification, or their complements or fragments, and
XX encoding at least 8 amino acids of any of the 6888 amino acid sequences
XX fully defined in the specification. The probe is a single exon probe that
XX hybridises under high stringency conditions to a nucleic acid molecule
XX expressed in human cells or tissues. Also included are a spatially-
XX addressable set of single exon nucleic acid probes for measuring human
XX gene expression (comprising a plurality of single exon nucleic acid
XX probes cited above, where each of the plurality of probes is separately
XX and addressably isolatable or amplifiable from the plurality), a single
XX exon microarray for measuring human gene expression, a method of
XX measuring human gene expression, a vector comprising the single exon
XX probe cited above, an ORF-encoded peptide comprising at least 8
XX contiguous amino acids of any of the above-mentioned amino acid
XX sequences (optionally with conservative amino acid substitutions), an
XX isolated antibody that binds specifically to a peptide cited above,
XX a customer desiring to measure gene expression, a method of providing
XX human gene expression data by subexpression, and a computer-readable
XX storage medium which contains a database having a plurality of records
XX (each record including data on the expression of a single exon probe
XX cited above. The probe, methods and apparatus are useful in gene
XX expression analysis. The probes may be used as tools for surveying
XX tissues to detect the presence of expressed messages that contain their
XX specific exon, or in constructing genome-derived single exon microarrays.
XX In addition, the probes are used in identifying and characterising
XX alternative splicing events, in detecting and characterising gross
XX alterations in the genomic locus that includes their exon, in assessing
XX smaller genomic alterations, in priming the synthesis of nucleic acids
XX or in expressing the ORF-encoded peptide. The present sequence is a human
XX single exon probe of the invention. Note: The present sequence is a human
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html?DocID=20030194704
XX Sequence 595 BP; 145 A; 163 C; 127 G; 160 T; 0 U; 0 Other;
Query Match 84.0%; Score 16.8; DB 12; Length 595;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AGGGCGTCTCTGAGTAGCAG 20
Db 422 AGGGCATCTCTGAGTTGCAG 403
RESULT 18
```

```
AAH19499
ID AAH19499 standard; cDNA; 775 BP.
XX
AC AAH19499;
XX
DT 03-AUG-2001 (first entry)
XX
DE Human galectin 15 coding sequence.
XX
KW Human; galectin 15; cytostatic; antiinflammatory; immunomodulatory;
KW haemostatic; anti-HIV; gene therapy; malignant tumour; haemopathy;
KW HIV infection; immunological disease; inflammation; ss.
XX
OS Homo sapiens.
XX
PN WO200130837-A1.
XX
PD 03-MAY-2001.
XX
PF 27-OCT-2000; 2000WO-CN000376.
XX
PR 28-OCT-1999; 99CN-00119900.
XX
PA (SHAN-) SHANGHAI BIO ROAD GENE DEV LTD.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2001-291028/30.
DR P-PSDB; AAB84886.
XX
PT Human galectin 15 and its encoding polynucleotides are applicable in
PT diagnosis and treatment of malignant tumors, hemopathy, HIV infection,
PT immunological diseases and various inflammations.
XX
PS Claim 6; Page 21; 28pp; Chinese.
XX
CC The present sequence is the coding sequence for human galectin 15.
CC Galectin 15 is useful in diagnosis and treatment of malignant tumour,
CC haemopathy, HIV infection, immunological diseases and inflammation
XX
SQ Sequence 775 BP; 209 A; 195 C; 170 G; 201 T; 0 U; 0 Other;
Query Match 84.0%; Score 16.8; DB 5; Length 775;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AGGGCGTCTCTGAGTAGCAG 20
Db 128 AGGGCATCTCTGAGTTGCAG 147
RESULT 19
ID ABD33213
XX ABD33213 standard; DNA; 80105 BP.
XX
AC ABD33213;
XX
DT 18-NOV-2004 (first entry)
XX
DE Murine cancer-associated (CA) gene MD07-034.
XX
KW Mouse; cancer-associated protein; CAP; cancer-associated gene; CA; gene;
KW ds; cancer; cytostatic.
XX
OS Mus musculus.
XX
PN WO2004058146-A2.
XX
PD 15-JUL-2004.
XX
PF 15-DEC-2003; 2003WO-US040081.
XX
PR 17-DEC-2002; 2002US-00322281.
```

XX (SAGR-) SAGRES DISCOVERY INC.
 XX Morris DW, Malandro MS;
 XX WPI; 2004-499109/47.
 XX Novel human cancer associated protein encoded within open reading frame
 XX of cancer associated gene, useful as targets for diagnosing cancer.
 XX Disclosure; SEQ ID NO 223; 182pp; English.
 XX The invention relates to cancer-associated proteins (CAP) and the cancer-
 XX associated (CA) nucleic acids encoding them. The invention also relates
 XX to a method for treating cancers involving administering to a patient an
 XX inhibitor of CAP, and a method of screening for anticancer activity in a
 XX potential drug involving providing a cell that expresses a CA gene,
 XX contacting a tissue sample derived from a cancer cell with an anticancer
 XX drug candidate and monitoring the effect of the anticancer drug candidate
 XX on expression of the CA gene. The CAP proteins are useful for detecting
 XX cancer associated with expression of a CAP protein in a test cell sample
 XX and for screening for a bioactive agent capable of modulating the
 XX activity of a CAP protein. The CA nucleic acids are useful for diagnosing
 XX cancer, involving determining the expression of a CA nucleic acid in a
 XX tissue. This sequence represents a murine CA gene of the invention. Note:
 XX The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic format directly from WIPO
 XX at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 80105 BP; 17052 A; 21395 C; 22145 G; 18961 T; 0 U; 552 Other;
 XX Query Match 84.0%; Score 16.8; DB 13; Length 80105;
 XX Best Local Similarity 90.0%; Pred. No. 2.7e+02;
 XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AGGGCTCTCTGAGTAGCAG 20
 DB 32700 AGGGCTACTCTGAGTAGCAG 32719
 RESULT 20
 AX98492
 ID AAX98492 standard; cDNA; 300 BP.
 XX AAX98492;
 XX 24-SEP-1999 (first entry)
 XX Human cancer cell derived cDNA #218.
 XX Cancer; human; colon; breast; lung; transmembrane receptor; ATPase;
 XX integral membrane protein; aspartyl protease; GATA family; wnt family;
 XX transcription factor; G-protein alpha subunit; protein phosphatase;
 XX phospholipase C; tyrosine phosphatase; diacylglycerol binding protein; trypsin;
 XX protein kinase; tyrosine phosphatase; developmental signalling protein;
 XX WW/rsp5/WMP domain; therapy; forensic; genetic mapping; diagnostic;
 XX detection; treatment; cervical; melanoma; colorectal adenocarcinoma;
 XX Wilm's tumour; retinoblastoma; sarcoma; myosarcoma; lung carcinoma;
 XX leukemia; lymphoma; dysplasia; hyperplasia; endometrium; adrenal;
 XX prostate; ss.
 XX Homo sapiens.
 XX WO9333982-A2.
 XX 08-JUL-1999.
 XX 22-DEC-1998; 98WO-US027610.
 XX 23-DEC-1997; 97US-0068755P.
 XX 03-APR-1998; 98US-0080664P.
 XX 21-OCT-1998; 98US-0105234P.
 XX 27-OCT-1998; 98US-0105877P.

PR 21-DEC-1998; 98US-00217471.
 XX (CHIR) CHIRON CORP.
 XX (HYSE-) HYSEQ INC.
 XX Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
 XX Reinhard C, Giese K, Randazzo F, Kennedy GC, Pot D, Kassam A;
 XX Lamson G, Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
 XX Leshkowitz D, Kita D, Garcia V, Jones LW, Stache-Crain B;
 XX WPI; 1999-430243/36.
 XX New isolated human polynucleotides.
 XX Claim 1; Page 370; 591pp; English.
 XX This invention describes novel isolated human polynucleotides obtained by
 XX screening for differential expression in colon cancer, breast cancer and
 XX lung cancer cell lines. The polynucleotides of the invention are
 XX represented in AAX98275-X99118 and encode polypeptides of protein
 XX families selected from 4 transmembrane segments integral membrane
 XX proteins, 7 transmembrane receptors, ATPases associated with various
 XX cellular activities (AAA), eukaryotic aspartyl proteases, GATA family of
 XX transcription factors, G-protein alpha subunit, phospholipase C or
 XX diacylglycerol binding proteins, protein kinase, protein phosphatase 2C,
 XX protein tyrosine phosphatase, trypsin, wnt family of developmental
 XX signalling proteins and WW/rsp5/WMP domain containing proteins. The
 XX encoded polypeptides also have a functional domain selected from Ank
 XX repeat, basic region plus leucine zipper transcription factors,
 XX bromodomain, EF-hand, SH3 domain, WD domain/G-beta repeats, zinc finger
 XX (C2H2 type), zinc finger (CCHC class), and zinc-binding metalloprotease
 XX domain. The polynucleotides encode polypeptides with similarity to known
 XX protein families and are predicted to have similar properties. The novel
 XX polynucleotides can be used to develop products for use as therapeutic
 XX agents and in forensics, genetic analysis, mapping and diagnostic
 XX applications. In particular, the product can be used for the detection
 XX and management of cancers. They can be used for treating e.g. cervical
 XX cancers, melanomas, colorectal adenocarcinomas, Wilm's tumour, sarcomas,
 XX retinoblastoma, myosarcomas, lung carcinomas, leukemias, such as chronic
 XX myelogenous leukemia, promyelocytic leukemia, monocytic leukemia, and
 XX myeloid leukemia, and lymphomas such as histiocytic lymphoma, anhydric
 XX hereditary ectodermal dysplasia, congenital alveolar dysplasia,
 XX epithelial dysplasia of the cervix, fibrous dysplasia of bone, and
 XX mammary dysplasia, hyperplasias, e.g. endometrial, adrenal, breast,
 XX prostate or thyroid hyperplasias or pseudoepitheliomatous hyperplasia of
 XX the skin
 XX SQ Sequence 300 BP; 58 A; 88 C; 99 G; 55 T; 0 U; 0 Other;
 Query Match 82.0%; Score 16.4; DB 2; Length 300;
 Best Local Similarity 94.4%; Pred. No. 2.4e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 GGCGTCTCTGAGTAGCAG 20
 DB 222 GGCGTCTCTGAGTAGCAG 239
 RESULT 21
 AAX99116
 ID AAX99116 standard; cDNA; 452 BP.
 XX AAX99116;
 XX 24-SEP-1999 (first entry)
 XX Human cancer cell derived cDNA contig #42.
 XX Cancer; human; colon; breast; lung; transmembrane receptor; ATPase;
 XX integral membrane protein; aspartyl protease; GATA family; wnt family;
 XX transcription factor; G-protein alpha subunit; protein phosphatase;
 XX phospholipase C; tyrosine phosphatase; diacylglycerol binding protein; trypsin;
 XX protein kinase; tyrosine phosphatase; developmental signalling protein;

CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 748 BP; 170 A; 209 C; 194 G; 175 T; 0 U; 0 Other;

Query Match 82.0%; Score 16.4; DB 12; Length 748;
Best Local Similarity 94.4%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGGTCTCTGAGTAGCAG 20
||||| ||||| ||||| |||||
Db 235 GCGGTCTCTGAGTAGCAG 218

RESULT 23
ADB62940
ID ADB62940 standard; cDNA; 1611 BP.
XX
AC ADB62940;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human cDNA encoding clone PLACB60132320.
XX
KW Human; ss; gene; pharmaceutical; diagnostic; gene therapy;
KW tissue regeneration; cell regeneration; membrane protein;
KW signal transduction-related protein; transcription-related protein;
KW osteoporosis; neurological disease; cancer; tumour.
XX
OS Homo sapiens.

XX FH Key Location/Qualifiers
XX CDS 471..1121
XX FT /*tag= a
XX FT /product= "Clone PLACB60132320 protein"
XX
PN EP1308459-A2.
XX
PD 07-MAY-2003.
XX
PF 28-MAR-2002; 2002EP-00007401.
XX
PR 05-NOV-2001; 2001JP-00379298.
PR 25-JAN-2002; 2002US-00350978.
XX
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tameschika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2003-450961/43.
DR P-PSDB; ADB64910.

XX New polynucleotides and polypeptides, useful for developing a diagnostic
PT marker or medicines for regulation of their expression and activity, or
PT as targets of gene therapy.
XX
PS Claim 1; Page; 222pp; English.

XX The invention discloses a polynucleotide comprising a sequence selected
CC from 1970 fully defined nucleotide sequences which encode novel
CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
CC or its partial peptide, an antibody binding to the polypeptide or peptide
CC of the polynucleotide, immunologically assaying the polypeptide or
CC peptide of the polynucleotide by contacting the polypeptide or peptide
CC with the antibody of the encoded protein, and observing the binding
CC between the two, a transformant carrying the polynucleotide in an
CC expressible manner and an antisense polynucleotide. The oligonucleotide
CC is useful as a primer for synthesising the polynucleotide, or as a probe
CC for detecting the polynucleotide. The polynucleotides and encoded
CC proteins are useful as pharmaceutical agents and many disease-related
CC genes may be included in them, for developing a diagnostic marker or

CC medicines for regulation of their expression and activity, or as targets
CC of gene therapy. The genes are involved in tissue and/or cell
CC regeneration. Membrane proteins, signal transduction-related proteins,
CC transcription-related proteins, disease-related proteins and genes
CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
CC neurological diseases, cancer, tumours. The cDNA may be used to regulate
CC the activity or expression of the encoded protein to treat diseases. The
CC sequence presented is a cDNA of the invention. Note: Some of the sequence
CC data for this patent is not represented in the printed specification, but
CC is based on sequence information supplied by the European Patent Office.
XX
SQ Sequence 1611 BP; 333 A; 435 C; 516 G; 327 T; 0 U; 0 Other;

Query Match 82.0%; Score 16.4; DB 10; Length 1611;
Best Local Similarity 94.4%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGGTCTCTGAGTAGCAG 20
||||| ||||| ||||| |||||
Db 636 GCGGTCTCTGAGTAGCAG 653

RESULT 24
AAC77862
ID AAC77862 standard; cDNA; 1992 BP.
XX
AC AAC77862;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human cancer associated gene sequence SEQ ID NO:256.
XX
KW Human; cancer associated gene; cancer antigen; detection; cancer;
KW diagnosis; cytostatic; proliferative; cancer; immunomodulator;
KW antidiabetic; antiaesthetic; antirheumatic; antiallergic; antiviral;
KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiac;
KW dermatological; neuroprotective; thrombolytic; coagulant; neotropic;
KW vasotropic; antipsoriatic; angiogenic; gene therapy; inflammation;
KW immune disorder; haematopoietic cell disorder; autoimmune disorder;
KW allergic reaction; graft versus host disease; organ rejection;
KW haemostatic; thrombolytic; cardiovascular disorder; infection;
KW neurological disease; drug screening; ss.

XX OS Homo sapiens.
XX PN WO200055350-A1.
XX
XX 21-SEP-2000.
XX
XX 08-MAR-2000; 2000WO-US005882.
XX
XX 12-MAR-1999; 99US-0124270P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX
XX WPI; 2000-587533/55.
XX P-PSDB; AAB43653.
XX
XX Novel isolated nucleic acids comprising sequences encoding peptides
PT useful for treating or diagnosing e.g. cancer.

XX Claim 1; Page 821-822; 2352pp; English.
XX
XX AAC77607 to AAC78448 encode the human cancer associated proteins given in
CC AAB43398 to AAB44239. The proteins can have activities based on the
CC tissues and cells the genes are expressed in. Example of activities
CC include: cytostatic; proliferative; cancer; immunomodulator;
CC antidiabetic; antiaesthetic; antirheumatic; antiallergic;
CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
CC dermatological; neuroprotective; cardiac; thrombolytic; coagulant;
CC neotropic; vasotropic; antipsoriatic and angiogenic. The

CC polynucleotides and polypeptides can be used for preventing, treating or
 CC ameliorating medical conditions and diagnosing pathological conditions.
 CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
 CC the present invention may be used to treat immune disorders by activating
 CC or inhibiting the proliferation, differentiation or mobilisation of
 CC immune cells, to treat disorders of haematopoietic cells, autoimmune
 CC disorders, allergic reactions, graft versus host disease and organ
 CC rejection, modulate haemostatic or thrombolytic activity, modulate
 CC inflammation, cancers, cardiovascular disorders, neurological disease and
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,
 CC agonists and antagonists may be also be used in drug screens. AAC78449 to
 CC AAC78457 and AAB44240 represent sequences used in the exemplification of
 CC the present invention

XX
 SQ Sequence 1992 BP; 396 A; 573 C; 628 G; 389 T; 0 U; 6 Other;

Query Match 82.0%; Score 16.4; DB 3; Length 1992;
 Best Local Similarity 94.4%; Pred. No. 2.9e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGCTCTCTGAGTAGCAG 20
 |||||
 Db 631 GCGCTCTCTGAGTAGCAG 648

RESULT 25
 AAH17632
 ID AAH17632 standard; cDNA; 2057 BP.

XX
 AC AAH17632;

XX
 DT 26-JUN-2001 (first entry)

XX
 DE Human cDNA sequence SEQ ID NO:17166.

XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX Homo sapiens.

OS
 XX EP1074617-A2.

XX
 PD 07-FEB-2001.

XX
 PF 28-JUL-2000; 2000EP-00116126.

XX
 PR 29-JUL-1999; 99JP-00248036.

PR 27-AUG-1999; 99JP-00300253.

PR 11-JAN-2000; 2000JP-00118776.

PR 02-MAY-2000; 2000JP-00183767.

PR 09-JUN-2000; 2000JP-00241899.

XX
 PA (HELI-) HELIX RES INST.

XX
 PI Ora T, Isogai T, Nishikawa T, Hayaehi K, Saito K, Yamamoto J;

PI Ieshii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX
 DR WPI; 2001-318749/34.

XX
 PS Claim 8; SEQ ID NO 17166; 2537pp + Sequence Listing; English.

XX The present invention describes primer sets for synthesising 5602 full-
 CC length cDNAs defined in the specification. Where a primer set comprises:
 CC (a) an oligo-dr primer and an oligonucleotide complementary to the
 CC complementary strand of a polynucleotide which comprises one of the 5602
 CC nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end

CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesising polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
 CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
 CC oligonucleotides, all of which are used in the exemplification of the
 CC present invention

XX
 SQ Sequence 2057 BP; 409 A; 594 C; 642 G; 412 T; 0 U; 0 Other;

Query Match 82.0%; Score 16.4; DB 4; Length 2057;
 Best Local Similarity 94.4%; Pred. No. 3e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGCTCTCTGAGTAGCAG 20
 |||||
 Db 1082 GCGCTCTCTGAGTAGCAG 1099

RESULT 26

ADP83544

ID ADP83544 standard; cDNA; 2250 BP.

XX
 AC ADP83544;

XX
 DT 26-FEB-2004 (first entry)

XX
 DE Human GRIM1 cDNA.

XX GRIM1; global repressor involved in myogenic differentiation; vulnery;
 KW muscular degeneration; muscle formation; skeletal muscle differentiation;
 KW fat cell differentiation; degenerative muscle disease; muscle injury; ss;
 KW gene; chromosome lp33.36.

XX
 OS Homo sapiens.

PH Key Location/Qualifiers

FT CDS 1..2250

FT /tag= a

FT /product= "GRIM-1"

XX
 PN WO2003078463-A1.

XX
 PD 25-SEP-2003.

XX
 PF 13-MAR-2003; 2003WO-EP002638.

XX
 PR 20-MAR-2002; 2002DE-01012397.

XX
 PA (UNIV-) UNIVERSITAETSKLINIKUM FREIBURG.

XX
 PI Schuele R, Hublitz P;

XX
 DR WPI; 2003-767506/72.

XX
 DR P-PSDB; ADF83530.

XX New global repressor involved in myogenic differentiation protein, useful
 PT for treating disorders of skeletal muscle and fat cell differentiation,
 PT also related cDNA and antibodies.

XX
 PS Claim 15; SEQ ID NO 1; 103pp; German.

XX This invention describes a novel polypeptide that includes a sequence of
 CC at least 20 consecutive amino acids of human or murine GRIM (Global
 CC repressor involved in myogenic differentiation)-1. The human GRIM1-
 CC encoding sequence is known, deposited as AL050019, and the corresponding

CC murine sequence has been identified by comparative screening of murine
 CC expressed sequence tags (EST's). The products of the invention have
 CC vulnary activity and the method of the invention can be used to modify
 CC GRIM function, by blocking movement of GRIM between nucleus and
 CC cytoplasm, to counteract existing muscular degeneration or activate
 CC muscle formation. GRIM is a repressor of many complexes or promoters.
 CC The GRIM polypeptides are used to treat disorders of skeletal muscle
 CC differentiation or fat cell differentiation, including degenerative
 CC muscle diseases and muscle injuries in the elderly and to identify
 CC specific modulators. This sequence encodes the human GRIM1 protein.
 CC
 SQ Sequence 2250 BP; 490 A; 639 C; 720 G; 401 T; 0 U; 0 Other;
 Query Match 82.0%; Score 16.4; DB 10; Length 2250;
 Best Local Similarity 94.4%; Pred. No. 3e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 GCGGTCTCTGAGTAGCAG 20
 Db 1780 GCGGTCTCTGAGTAGCAG 1797
 RESULT 27
 ACN37249
 ID ACN37249 standard; cDNA; 2508 BP.
 AC ACN37249;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Tumour-associated antigenic target (TAT) cDNA DNA323721, SEQ ID NO:6.
 XX
 KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
 KW tumour; diagnosis; cell proliferative disorder; breast cancer;
 KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
 KW central nervous system cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; melanoma; leukaemia; hybridisation probe;
 KW chromosome identification; chromosome mapping; gene mapping;
 KW gene therapy; cytostatic; gene; ss.
 OS Homo sapiens.
 XX
 XX WO2004030615-A2.
 PN
 XX
 PD 15-APR-2004.
 XX
 PF 29-SEP-2003; 2003WO-US028547.
 XX
 PR 02-OCT-2002; 2002US-0414971P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Wu TD, Zhang Z, Zhou Y;
 XX
 XX WPI; 2004-347921/32.
 DR
 DR P-PSDB; ABM80001.
 XX
 XX New tumor-associated antigenic target polypeptides and nucleic acids,
 PT useful in preparing a medicament for treating or detecting a
 PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
 PT prostate cancer or tumor.
 XX
 PS Claim 1; SEQ ID NO 6; 7273pp; English.
 XX
 CC The invention relates to human tumour-associated antigenic target (TAT)
 CC polypeptides, and their related nucleic acids. The TAT polypeptides are
 CC overexpressed in cancer tissues compared to normal tissues, and may thus
 CC serve as effective targets for the diagnosis and treatment of cancer in
 CC mammals. The invention also relates to nucleic acid and polypeptide
 CC sequences at least 80% identical to the TAT nucleic acids and
 CC polypeptides; expression vectors and host cells comprising a TAT nucleic
 CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
 CC molecule which binds to a TAT polypeptide; fusion proteins comprising a

CC TAT polypeptide; and methods and compositions for the treatment or
 CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
 CC antibodies, antagonists, binding molecules and compositions are useful
 CC for diagnosing or treating a cell proliferative disorder associated with
 CC increased TAT expression, particularly cancers such as breast cancer,
 CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
 CC cancer, pancreatic cancer, cervical cancer, cancers of the central
 CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
 CC used as hybridisation probes, in chromosome and gene mapping, in
 CC chromosome identification and in gene therapy. The present sequence
 CC represents a TAT nucleic acid of the invention
 XX

SQ Sequence 2508 BP; 534 A; 705 C; 782 G; 487 T; 0 U; 0 Other;

Query Match 82.0%; Score 16.4; DB 13; Length 2508;

Best Local Similarity 94.4%; Pred. No. 3e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGGTCTCTGAGTAGCAG 20

Db 1548 GCGGTCTCTGAGTAGCAG 1565

RESULT 28

ABL90233/c

ID ABL90233 standard; cDNA; 2665 BP.

XX ABL90233;

AC ABL90233;

XX

DT 24-MAY-2002 (first entry)

XX

DE Human polynucleotide SEQ ID NO 795.

XX

XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
 KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein; gene; ss.

OS Homo sapiens.

XX

XX WO200190304-A2.

PN

XX

PD 29-NOV-2001.

XX

PF 18-MAY-2001; 2001WO-US016450.

XX

PR 19-MAY-2000; 2000US-0205515P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Birse CE, Rosen CA;

XX

XX WPI; 2002-122018/16.

DR

DR P-PSDB; ABB89824.

XX

XX Novel 1405 isolated polypeptides, useful for diagnosis, treatment and

PT prevention of neural, immune system, muscular, reproductive,

PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative

PT disorders.

XX

PS Claim 4; SEQ ID NO 795; 2081pp + Sequence Listing; English.

XX

XX The invention relates to novel genes (ABL89449-ABL90853) and proteins

CC (ABB9040-ABB90444) useful for preventing, treating or ameliorating

CC medical conditions e.g. by protein or gene therapy. The genes are

CC isolated from a range of human tissues disclosed in the specification.

CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in

CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and

CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,

CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune

CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic

CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,

CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)
 CC
 XX Sequence 2665 BP; 518 A; 846 C; 746 G; 550 T; 0 U; 5 Other;
 SQ

Query Match 82.0%; Score 16.4; DB 6; Length 2665;
 Best Local Similarity 94.4%; Pred. No. 3e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGCTCTCTGAGTAGCAG 20
 |||||
 Db 1169 GCGCTCTCTGAGTAGCAG 1152

RESULT 29
 AAH18559
 ID AAH18559 standard; cDNA; 2753 BP.
 XX
 AC AAH18559;
 XX
 DT 26-JUN-2001 (first entry)
 XX
 DE Human cDNA sequence SEQ ID NO:18728.
 XX
 KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1074617-A2.
 XX
 PD 07-FEB-2001.
 XX
 PF 28-JUL-2000; 2000EP-00116126.
 XX
 PR 29-JUL-1999; 99JP-00248036.
 PR 27-AUG-1999; 99JP-00300253.
 PR 11-JAN-2000; 2000JP-00118776.
 PR 02-MAY-2000; 2000JP-00183767.
 PR 09-JUN-2000; 2000JP-00241899.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isogai T, Nishikawa T, Hayaashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX
 DR WPI; 2001-318749/34.
 XX
 PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
 PT length cDNAs defined in the specification, and for the detection and/or
 PT diagnosis of the abnormality of the proteins encoded by the full-length
 PT cDNAs.
 XX
 PS Claim 8; SEQ ID NO 18728; 2537pp + Sequence Listing; English.
 XX
 CC The present invention describes primer sets for synthesising 5602 full-
 CC length cDNAs defined in the specification. Where a primer set comprises:
 CC (a) an oligo-dr primer and an oligonucleotide complementary to the
 CC complementary strand of a polynucleotide which comprises one of the 5602
 CC nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesising polynucleotides,
 CC

CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893
 CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
 CC oligonucleotides, all of which are used in the exemplification of the
 CC present invention
 XX
 SQ Sequence 2753 BP; 580 A; 775 C; 872 G; 526 T; 0 U; 0 Other;
 Query Match 82.0%; Score 16.4; DB 4; Length 2753;
 Best Local Similarity 94.4%; Pred. No. 3e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGCTCTCTGAGTAGCAG 20
 |||||
 Db 1793 GCGCTCTCTGAGTAGCAG 1810

RESULT 30
 AAH72382
 ID AAH72382 standard; cDNA; 2781 BP.
 XX
 AC AAH72382;
 XX
 DT 19-DEC-2000 (first entry)
 XX
 DE Human nucleic acid-binding protein NuABP-1 cDNA.
 XX
 KW Human nucleic acid-binding protein; NuABP; agonist; antagonist; EST;
 KW expressed sequence tag; drug screening; recombinant expression; antibody;
 KW reproductive disorder; infertility; immunological disorder;
 KW neurological disorder; cell proliferative disorder; cancer; tumour; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2000044900-A2.
 XX
 PD 03-AUG-2000.
 XX
 PF 28-JAN-2000; 2000WO-US002237.
 XX
 PR 29-JAN-1999; 99US-0117904P.
 PR 29-JAN-1999; 99US-0117905P.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Tang YT, Lal P, Hillman JL, Yue H, Azimzai Y, Lu AMD, Baughn MR;
 PI Tran B, Shih LL, Au-Young JL;
 XX
 DR WPI; 2000-499332/44.
 DR P-PSDB; AAB20997.
 XX
 PT Novel nucleic acid binding proteins, used to identify agonists and
 PT antagonists of them, for the treatment of reproductive, immunological,
 PT neurological and cell proliferative disorders including cancer.
 XX
 PS Claim 4; Page 145; 180pp; English.
 XX
 CC Sequences AAH72382-A72436 represent cDNAs encoding novel human nucleic
 CC acid-binding proteins (NuABPs; AAB20997-B21051). These cDNAs were
 CC produced by extension from an appropriate EST (expressed sequence tag)
 CC using primers designed using the EST. The invention also relates to
 CC expression constructs, host cells and transgenic organisms comprising a
 CC human NuABP nucleic acid, recombinant production of the human NuABPs, and
 CC antibodies against the human NuABPs, and also to methods of screening
 CC modulators of human NuABP activity or expression. The human NuABPs, and
 CC their agonists and antagonists are used to treat diseases associated with
 CC overexpression or underexpression of functional NuABPs. Human NuABP
 CC proteins and nucleotides, and NuABP agonists and antagonists can be used
 CC to diagnose, treat and prevent reproductive, immunological, neurological
 CC and cell proliferative disorders. Reproductive disorders that may be

CC treated using compositions of the invention include infertility,
 CC endometriosis, disruptions of the menstrual cycle and disruptions of
 CC spermatogenesis. Immunological disorders that may be treated include
 CC AIDS, allergies, and autoimmune disorders such as multiple sclerosis,
 CC rheumatoid arthritis, diabetes and systemic lupus erythematosus.
 CC Neurological disorders that may be treated include epilepsy, and
 CC neurodegenerative conditions such as Alzheimer's disease and Parkinson's
 CC disease, prion diseases such as Creutzfeldt-Jakob disease, and mental
 CC disorders such as schizophrenia. Cell proliferative disorders that may be
 CC treated include a wide variety of cancers, and also arteriosclerosis,
 CC atherosclerosis, cirrhosis and psoriasis
 XX
 SQ Sequence 2781 BP; 594 A; 779 C; 881 G; 527 T; 0 U; 0 Other;

Query Match 82.0%; Score 16.4; DB 3; Length 2781;
 Best Local Similarity 94.4%; Pred. No. 3.1e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 GCGCTCTCTGAGTACGAG 20
 |||||
 Db 1810 GCGCTCTCTGAGCAGCAG 1827

RESULT 31
 AAKS2536/c
 ID AAKS2536 standard; cDNA; 3163 BP.

XX AC AAKS2536;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polynucleotide SEQ ID NO 2065.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation; ss.

XX OS Homo sapiens.
 XX
 PN WO200157190-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001WO-US004098.
 XX
 PR 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 PR 20-JUN-2000; 2000US-00598075.
 PR 19-JUL-2000; 2000US-00620325.
 PR 01-SEP-2000; 2000US-00654936.
 PR 15-SEP-2000; 2000US-00663561.
 PR 20-OCT-2000; 2000US-00693325.
 PR 30-NOV-2000; 2000US-00728422.

XX (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
 PI Ma Y, Zhao QH, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX
 DR WPI; 2001-476283/51.
 DR P-PSDB; AAM79403.

XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
 PT in diagnosis and gene therapy.

PS Claim 1; Page 4450-4451; 6221pp; English.

XX The invention relates to polynucleotides (AAKS1456-AAKS3435) and the
 CC encoded polypeptides (AAM78323-AAW80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The

CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAKS2581), 2111
 CC (AAKS2582) and 3666 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication
 XX
 SQ Sequence 3163 BP; 611 A; 1008 C; 900 G; 644 T; 0 U; 0 Other;

Query Match 82.0%; Score 16.4; DB 4; Length 3163;
 Best Local Similarity 94.4%; Pred. No. 3.1e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGCTCTCTGAGTACGAG 20
 |||||
 Db 1349 GCGCTCTCTGAGCAGCAG 1332

RESULT 32
 AAKS1552
 ID AAKS1552 standard; cDNA; 3236 BP.

XX AC AAKS1552;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polynucleotide SEQ ID NO 97.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation; ss.

XX OS Homo sapiens.
 XX
 PN WO200157190-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001WO-US004098.

XX 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 PR 20-JUN-2000; 2000US-00598075.
 PR 19-JUL-2000; 2000US-00620325.
 PR 01-SEP-2000; 2000US-00654936.
 PR 15-SEP-2000; 2000US-00663561.
 PR 20-OCT-2000; 2000US-00693325.
 PR 30-NOV-2000; 2000US-00728422.

XX (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
 PI Ma Y, Zhao QH, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX
 DR WPI; 2001-476283/51.
 DR P-PSDB; AAM78419.

XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
 PT in diagnosis and gene therapy.

PS Claim 1; Page 717-720; 6221pp; English.

XX The invention relates to polynucleotides (AAKS1456-AAKS3435) and the
 CC encoded polypeptides (AAM78323-AAW80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,

CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication

XX
 SQ Sequence 3236 BP; 656 A; 924 C; 1040 G; 613 T; 0 U; 3 Other;

Query Match 82.0%; Score 16.4; DB 4; Length 3236;
 Best Local Similarity 94.4%; Pred. No. 3.1e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGCTCTCTGAGTAGCAG 20
 |||||
 DB 1872 GCGCTCTCTGAGTAGCAG 1889

RESULT 33
 AAC75812
 ID AAC75812 standard; cDNA; 3619 BP.
 AC AAC75812;
 DT 08-FEB-2001 (first entry)
 DE Human ORFX ORF1367 polynucleotide sequence SEQ ID NO:2733.

XX Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
 XX vulnery; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antinflammatory;
 KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
 KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antinflammatory disease; coagulation;
 KW thrombosis; contraceptive; SS.

XX Homo sapiens.
 OS
 XX WO200058473-A2.
 PN
 XX 05-OCT-2000.
 PD
 XX 31-MAR-2000; 2000WO-US008621.
 XX
 XX 31-MAR-1999; 99US-0127607P.
 PR
 PR 02-APR-1999; 99US-0127636P.
 PR
 PR 05-APR-1999; 99US-0127728P.
 PR
 PR 30-MAR-2000; 2000US-00540763.
 XX
 XX (CURA-) CURAGEN CORP.
 PA
 XX Shimkets RA, Leach M;
 PI
 XX WPI; 2000-602362/57.
 DR
 DR P-PSDB; AAB41603.

XX Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease.
 XX
 XX Claim 5; Page 1974-1976; 5507pp; English.

XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnery;

CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
 CC anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
 CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
 CC dermatological; immunosuppressive; antinflammatory; antibacterial;
 CC antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The
 CC sequences can be used for determining the presence of or predisposition
 CC to, or preventing or treating pathological conditions associated with an
 CC ORFX-associated disorder. The nucleic acids can be used to express ORFX
 CC proteins in gene therapy vectors. The proteins and nucleic acids may be
 CC used to treat cancers, proliferative disorders, neurodegenerative
 CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
 CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
 CC storage, systemic lupus erythematosus, severe combined immunodeficiency
 CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
 CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
 CC cartilage damage, nocturnal haemoglobinuria, antinflammatory disease; to
 CC enhance coagulation; to inhibit thrombosis; and as a contraceptive
 XX
 SQ Sequence 3619 BP; 718 A; 1049 C; 1153 G; 696 T; 0 U; 3 Other;

Query Match 82.0%; Score 16.4; DB 3; Length 3619;
 Best Local Similarity 94.4%; Pred. No. 3.1e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGCTCTCTGAGTAGCAG 20
 |||||
 DB 2029 GCGCTCTCTGAGTAGCAG 2046

RESULT 34
 ADQ23383/c
 ID ADQ23383 standard; DNA; 4560 BP.
 XX ADQ23383;
 AC ADQ23383;
 XX
 DT 26-AUG-2004 (first entry)
 XX Human soft tissue sarcoma-upregulated DNA - SEQ ID 6203.

XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
 KW ds.
 KW
 XX Homo sapiens.
 OS
 XX WO2004048938-A2.
 PN
 XX 10-JUN-2004.
 PD
 XX 26-NOV-2003; 2003WO-US038193.
 PF
 XX 26-NOV-2002; 2002US-0429739P.
 PR
 XX (PROT-) PROTEIN DESIGN LABS INC.
 PA
 XX Aziz N, Ginsburg WM, Zlotnik A;
 PI
 XX WPI; 2004-441208/41.
 DR
 XX Early detection of soft tissue sarcoma comprises determining expression
 PT of a gene in a first soft tissue sample and a normal soft tissue sample
 PT and comparing the gene expression, also useful in treating soft tissue
 PT sarcoma.
 PT
 XX Example 2; SEQ ID NO 6203; 210pp; English.

XX The invention relates to a novel method for detecting soft tissue sarcoma
 CC which comprises obtaining a first soft tissue sample from an individual
 CC and a normal soft tissue sample from the same or different individual,
 CC determining the expression of a gene in both samples and comparing the
 CC expression of the gene in both soft tissue samples, where a higher level
 CC of protein expression in the first soft tissue sample indicates the
 CC presence of soft tissue sarcoma. The method of the invention has
 CC cytostatic applications and may be useful for detecting soft tissue

CC sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the CC specification per se but was submitted in CD format by the inventor.

XX Sequence 4560 BP; 803 A; 1537 C; 1370 G; 850 T; 0 U; 0 Other;

Query Match 82.0%; Score 16.4; DB 12; Length 4560;

Best Local Similarity 94.4%; Pred. No. 3.2e+02; Mismatches 17; Conservative 0; Indels 1; Gaps 0;

QY 3 GCGGCTCTCTGAGTAGCAG 20

DB 2727 GCGGCTCTCTGAGTAGCAG 2710

RESULT 35

ADP83532
ID ADF83532 standard; DNA; 15105 BP.

AC ADF83532;

DT 26-FEB-2004 (first entry)

XX Human GRIM1 DNA.

XX GRIM-1; global repressor involved in myogenic differentiation; vulneryary; muscular degeneration; muscle formation; skeletal muscle differentiation; fat cell differentiation; degenerative muscle disease; muscle injury; gene; ds; chromosome 1p33.36.

OS Homo sapiens.

PN WO2003078463-A1.

XX 25-SEP-2003.

PF 13-MAR-2003; 2003WO-EP002638.

PR 20-MAR-2002; 2002DE-01012397.

XX (UNIV-) UNIVERSITAETSKLINIKUM FREIBURG.

PI Schuele R, Hublitz P;

DR WPI; 2003-767506/72.

XX New global repressor involved in myogenic differentiation protein, useful for treating disorders of skeletal muscle and fat cell differentiation, also related cDNA and antibodies.

PS Example 6; SEQ ID NO 5; 103pp; German.

XX This invention describes a novel polypeptide that includes a sequence of at least 20 consecutive amino acids of human or murine GRIM1 (global repressor involved in myogenic differentiation). The human GRIM1-encoding sequence is known, deposited as AL050019, and the corresponding murine sequence has been identified by comparative screening of murine expressed sequence tags (EST's). The products of the invention have vulneryary activity and the method of the invention can be used to modify GRIM function, by blocking movement of GRIM between nucleus and cytoplasm, to contract existing muscular degeneration or activate muscle formation. GRIM is a repressor of many complexes and promoters. The GRIM polypeptides are used to treat disorders of skeletal muscle differentiation or fat cell differentiation, including degenerative muscle diseases and muscle injuries in the elderly and to identify specific modulators. This sequence encodes the human GRIM1 protein.

XX Sequence 15105 BP; 2767 A; 3992 C; 4967 G; 3379 T; 0 U; 0 Other;

Query Match 82.0%; Score 16.4; DB 10; Length 15105;

Best Local Similarity 94.4%; Pred. No. 3.7e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGGCTCTCTGAGTAGCAG 20

DB 12881 GCGGCTCTCTGAGTAGCAG 12898

RESULT 36

ADQ97081/c

ID ADQ97081 standard; DNA; 63411 BP.

XX ADQ97081;

DT 07-OCT-2004 (first entry)

XX Mouse cancer associated sequence MD10-004, SEQ ID 57.

XX Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Mouse; ds.

OS Mus musculus.

PN WO2004060304-A2.

XX 22-JUL-2004.

PF 22-DEC-2003; 2003WO-US041389.

PR 27-DEC-2002; 2002US-00330773.

PA (SAGR-) SAGRES DISCOVERY INC.

XX Morris DW, Malandro MS;

XX WPI; 2004-543781/52.

XX New isolated cancer associated nucleic acids comprising at least 10 contiguous nucleotides, useful for diagnosing, preventing and/or treating cancers such as leukemia and lymphoma.

PS Claim 1; SEQ ID NO 57; 199pp; English.

XX The present invention relates to cancer associated sequences (ADQ97025-ADQ98004). The sequences are useful for the diagnosis, prevention and/or treatment of cancer, such as leukemia and lymphoma. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 63411 BP; 17408 A; 15472 C; 14344 G; 15847 T; 0 U; 340 Other;

Query Match 82.0%; Score 16.4; DB 12; Length 63411;

Best Local Similarity 94.4%; Pred. No. 4.3e+02; Mismatches 17; Conservative 0; Indels 1; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGC 18

DB 29444 AGGGCTTCTCTGAGTAGC 29427

RESULT 37

ACH41376/c

ID ACH41376 standard; cDNA; 458 BP.

XX ACH41376;

DT 13-OCT-2003 (first entry)

XX Human foetal brain cDNA #2743.

XX Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.

OS Homo sapiens.

```

XX US2003073623-A1.
PN
XX
XX 17-APR-2003.
XX
XX 30-JUL-2001; 2001US-00918995.
XX
XX 30-JUL-2001; 2001US-00918995.
XX
XX (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
XX
XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
PI
XX
XX WPI; 2003-615964/58.
XX
XX New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX
XX Claim 1; SEQ ID NO 28588; 44pp; English.
XX
XX The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversity, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030073623
XX
XX Seq Sequence 458 BP; 104 A; 106 C; 120 G; 123 T; 0 U; 5 Other;
SQ
Query Match 79.0%; Score 15.8; DB 9; Length 458;
Best Local Similarity 89.5%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGCTCTCTGAGTAGCA 19
Db 253 AGGGCGCTCTCTGAGTAGCA 235

RESULT 38
AAH22902
ID AAH22902 standard; DNA; 525 BP.
XX
XX AAH22902;
AC
XX
XX 17-SEP-2001 (first entry)
DT
XX
XX Codon optimised mature hG-CSF protein encoding DNA.
DE
XX
XX Granulocyte-colony stimulating factor; G-CSF; hemotopoietic; AIDS;
KW chemotherapy; immunodeficiency disease; anti-HIV; cytostatic;
KW antibacterial; gene therapy; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 1. .525
FT CDS

/*tag= a
/product= "mature hG-CSF"

WO200151510-A2.
XX
XX 19-JUL-2001.
XX
XX 09-JAN-2001; 2001WO-DK000011.
XX
XX 10-JAN-2000; 2000DK-00000024.
PR 02-MAR-2000; 2000DK-00000341.
PR 16-JUN-2000; 2000DK-00000943.
XX
XX (MAXY-) MAXYGEN APS.
PA
XX
XX Nissen TL, Andersen KV, Hansen CK, Mikkelsen JM, Schambye HT;
PI
XX
XX WPI; 2001-451839/48.
XX
XX P-PSDB; AAB85332.
XX
XX Novel polypeptides exhibiting granulocyte-colony stimulating factor
PT activity and conjugates between the polypeptide and a non-polypeptide
PT moiety, useful for treating leukopenia, AIDS and bacterial or other
PT infections.
XX
XX Example 1; Page 92; 94pp; English.
XX
XX The invention provides a polypeptide (PP) conjugate (I) exhibiting
CC granulocyte-colony stimulating factor (G-CSF) activity, comprising PP
CC with an amino acid (aa) sequence that differs from aa sequence of human G
CC -CSF by at least one aa residue comprising an attachment group for a non-
CC PP group and having a non-PP group bound to attachment of PP and the
CC polypeptide (II) portion of (I) exhibiting G-CSF activity. (I) and (II)
CC are useful for treating general hemotopoietic disorders, including
CC disorders arising from radiation therapy or from chemotherapy, AIDS or
CC immunodeficiency diseases, leukopenia and bacterial or other infections.
CC (II) is useful for therapeutic, diagnostic and other purposes and in
CC particular finds use as intermediate products for preparation of (I). (I)
CC and (II) are used for preventing infection in cancer patients undergoing
CC radiation therapy, chemotherapy and bone marrow transplantations, to
CC mobilize progenitor cells for collection in peripheral blood progenitor
CC cell transplantations and to support treatment of patients with acute
CC myeloid leukemia. A nucleotide sequence encoding (II) is useful in gene
CC therapy applications. (I) has increased functional in vivo half-life,
CC increased serum half-life, reduced renal clearance, reduced receptor-
CC mediated clearance, reduced side effects, such as bone pain, reduced
CC immunogenicity and/or increased bioavailability. The present sequence
CC represents a DNA encoding a mature hG-CSF with its codon usage optimised
CC for expression in E. coli. This is used in the construction of synthetic
CC genes encoding hG-CSF
XX
XX Seq Sequence 525 BP; 104 A; 143 C; 153 G; 125 T; 0 U; 0 Other;
SQ
Query Match 79.0%; Score 15.8; DB 4; Length 525;
Best Local Similarity 89.5%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGCTCTCTGAGTAGCAG 20
Db 173 GGGCGCTCTCTGAGTAGCTG 191

RESULT 39
ADK41220
ID ADK41220 standard; DNA; 525 BP.
XX
XX ADK41220;
AC
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX DNA encoding human granulocyte colony-stimulating factor protein.
DE
XX
XX granulocyte colony-stimulating factor; G-CSF; immunostimulant; anti-HIV;
KW

```


virucide; antibacterial; fungicide; cytostatic; neutropenia; leukopenia; chemotherapy; radiation therapy; HIV; AIDS; immunodeficiency disease; bacterial infection; acute myeloid leukaemia; antifungal therapy; systemic; invasive candidiasis; human; hG-CSF; ds; gene.

Homo sapiens.

Key Location/Qualifiers
CDS 1..525
/*tag= a
/partial
/product= "Human granulocyte colony-stimulating factor protein"
/note= "No start codon"

WO2003006501-A2.

23-JAN-2003.

10-JUL-2002; 2002WO-DK000482.

11-JUL-2001; 2001US-00904196.

22-MAR-2002; 2002DK-00000447.

08-MAY-2002; 2002DK-00000708.

(MAXY-) MAXYGEN HOLDINGS LTD.

Nissen TL, Andersen KV, Hansen CK, Mikkelsen JM, Schambye HT;

WPI; 2003-221717/21.

P-PSDB; ADK41219.

New polypeptide conjugate exhibiting granulocyte colony-stimulating factor activity, useful for preventing or treating neutropenia or leukopenia due to chemotherapy or radiation therapy, AIDS or other immunodeficiency diseases.

Example 1; SEQ ID NO 2; 106pp; English.

The invention relates to a novel polypeptide conjugate exhibiting granulocyte colony-stimulating factor activity (G-CSF). The polypeptide conjugate comprises: a polypeptide comprising at least one substitution selected from the group of K16R/Q, K34R/Q, and K40R/Q, and at least one substitution selected from the group of T105K and S159K relative to the amino acid sequence of hG-CSF having a 174 residue amino acid sequence, given in the specification, or in a corresponding position relative to an amino acid sequence having at least 80 % sequence identity with the 174 residue amino acid sequence, where the conjugate has 2-6 polyethylene glycol moieties with a molecular weight of 1000-10000 Da attached to attachment groups of the polypeptide; or a polypeptide comprising an amino acid sequence that differs in at least one amino acid residue from the amino acid sequence of hG-CSF having the sequence of the 174 residue amino acid sequence, and with at least one non-polypeptide moiety attached to an attachment group of the polypeptide, where the conjugate has an in vitro bioactivity in the range of 2-30% of the bioactivity of non-conjugated hG-CSF as determined by the luciferase assay. The G-CSF conjugate has immunostimulant, anti-HIV, virucide, antibacterial, fungicide, and cytostatic activities. The polypeptide conjugate is useful as a pharmaceutical, or for preparing a pharmaceutical composition for treating an insufficient neutrophil level. The pharmaceutical composition is also useful for preventing and/or treating neutropenia or leukopenia due to chemotherapy or radiation therapy, or due to HIV or another viral infection. The polypeptide conjugate may also be used for treating AIDS or other immunodeficiency diseases, bacterial infections, acute myeloid leukaemia, or for antifungal therapy, particularly for treating systemic or invasive candidiasis. This polynucleotide sequence represents the DNA encoding the human G-CSF protein of the invention.

Sequence 525 BP; 104 A; 143 C; 153 G; 125 T; 0 U; 0 Other;

Query Match

Best Local Similarity 79.0%; Score 15.8; DB 10; Length 525;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGCTCTCGAGTAGCAG 20
||||| |||||||
DB 173 GGGCGCCTCTCGAGTAGCTG 191

RESULT 40

ABS52517

ID ABS52517 standard; DNA; 531 BP.

XX

AC ABS52517;

XX

DT 15-NOV-2002 (first entry)

XX

DE DNA encoding G-CSF copy 2 in the single chain G-CSF dimer.

XX

KW Gene; ds; single-chain multimeric polypeptide; polyethylene glycol; PEG; granulocyte colony stimulating factor; G-CSF; human; haematopoietic disorder; radiation therapy; chemotherapy; bone marrow transplantation; acquired immunodeficiency syndrome; AIDS; immunodeficiency disease; leukopenia; acute myeloid leukaemia; half-life; clearance; immunogenicity; bioavailability; single chain G-CSF dimer; antihuman immunodeficiency virus; HIV; haemostatic.

OS Homo sapiens.

OS Synthetic.

FH Key

CDS Location/Qualifiers

1..525

/*tag= a

/product= "G-CSF dimer"

/partial

/note= "This CDS encodes for residues 175-348 in the G-CSF dimer polypeptide. No start codon shown"

XX WO200236626-A1.

XX

XX 10-MAY-2002.

XX

XX 01-NOV-2001; 2001WO-DK000724.

XX

XX 02-NOV-2000; 2000DK-00001647.

XX

PA (MAXY-) MAXYGEN APS.

PA (MAXY-) MAXYGEN HOLDINGS LTD.

XX

PI Nissen TL, Jensen AD;

XX

XX WPI; 2002-618972/66.

XX

XX P-PSDB; ABG32020.

XX

PT Single chain multimeric polypeptide conjugate for treating hematopoietic disorders, has two units of monomeric polypeptides linked via peptide bond/linker and polymer group bound to attachment group of polypeptide.

XX

XX Example 1; Page 94; 108pp; English.

XX

CC The invention discloses a single-chain multimeric polypeptide conjugate comprising at least two units of a monomeric polypeptide linked via a peptide bond or a peptide linker, where the monomeric polypeptide is biologically active in its monomeric form and has at least one polymer group covalently bound to an attachment group of the polypeptide e.g. polyethylene glycol (PEG). The polypeptide is preferably a single-chain multimeric granulocyte colony stimulating factor (G-CSF) polypeptide comprising at least two G-CSF polypeptide monomers, linked via a peptide bond or a peptide linker, where at least one of the monomers is a variant of wild-type human G-CSF comprising at least one amino acid residue modification. The monomeric and multimeric polypeptides are useful in therapy and for manufacture of a medicament for treatment of general haematopoietic disorders, including disorders arising from radiation therapy, chemotherapy or bone marrow transplantations, acquired immunodeficiency syndrome (AIDS) or other immunodeficiency diseases, leukopenia and acute myeloid leukaemia. The conjugate has one or more

CC important properties as compared to the native polypeptide, including
 CC increased functional in vivo half-life, increased serum half-life,
 CC reduced clearance, reduced immunogenicity and/or increased
 CC bioavailability. Consequently, medical treatment with a conjugate offers
 CC advantages including longer duration between infections and fewer side
 CC effects. The sequence presented is the DNA encoding the G-CSF copy 2 in
 CC the single chain G-CSF dimer

XX SQ Sequence 531 BP; 106 A; 144 C; 154 G; 127 T; 0 U; 0 Other;

Query Match 79.0%; Score 15.8; DB 6; Length 531;
 Best Local Similarity 89.5%; Pred. No. 5.1e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGTCTCTGAGTAGCAG 20
 DB 173 GGGCGCTCTGAGTAGCTG 191

RESULT 41
 ABZ53961/c
 ID ABZ53961 standard; cDNA; 596 BP.

XX AC ABZ53961;
 XX DT 28-MAR-2003 (first entry)

DE DE Aspergillus oryzae polynucleotide SEQ ID NO 3074.

KW Aspergillus oryzae; fermentation; fungus; industrial; EST;
 KW expressed sequence tag; gene; ss.

XX OS Aspergillus oryzae.

XX PN WO200279476-A1.

XX PD 10-OCT-2002.

XX PF 22-MAR-2002; 2002WO-IB000890.

XX PR 30-MAR-2001; 2001JP-00098371.

XX PA (NARD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

XX PA (NORQ-) NAT INST BREWING.

XX PA (NORQ-) NAT FOOD RES INST MIN AGRIC.

XX PI Machida M, Akita O, Kashiwagi Y, Kitamoto K, Horiuchi H;

XX PI Takeuchi M, Kobayashi T, Kitamoto N, Gomi K, Abe K;

XX DR WPI; 2003-046817/04.

XX PT Detection of expression of specific Aspergillus genes for monitoring the
 PT fermentation and growth conditions of the fungus, using DNA probes.

XX PS Claim 1; SEQ ID NO 3074; 48pp + Sequence Listing; Japanese.

XX CC The invention relates to a polynucleotide having any of 6006 specific
 CC sequences (ABZ50888-ABZ56893), which are expressed by a fungus under
 CC specific culture conditions including one or more of eutrophic,
 CC oligotrophic, solid, early germination, alkaline, high temperature, low
 CC temperature or maltose culture or polynucleotides stringently hybridising
 CC to these sequences. The polynucleotides are useful for monitoring the
 CC progress of fermentation and the growth conditions of a fungus,
 CC especially of Aspergillus oryzae which is widely used in industrial
 CC fermentation. Also monitoring for fungal contamination. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 596 BP; 161 A; 153 C; 138 G; 144 T; 0 U; 0 Other;

Query Match 79.0%; Score 15.8; DB 8; Length 596;
 Best Local Similarity 89.5%; Pred. No. 5.2e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCA 19
 DB 495 AGGGCGCTCTTAAGTAGCA 477

RESULT 42

AAA01703/c

ID AAA01703 standard; cDNA; 779 BP.

XX AC AAA01703;

XX DT 19-MAY-2000 (first entry)

DE DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:1694.

KW Human; colon cancer; tumour; diagnosis; gene expression product; probe;
 KW detection; cancerous state; metastasis; identification; breast cancer;
 KW oestrogen receptor-positive breast cancer; therapy;
 KW oestrogen receptor-negative breast cancer; lung cancer; ss.

XX OS Homo sapiens.

XX PN WO9958675-A2.

XX PD 18-NOV-1999.

XX PF 13-MAY-1999; 99WO-US010602.

XX PR 14-MAY-1998; 98US-0085426P.

XX PR 15-MAY-1998; 98US-0085537P.

XX PR 15-MAY-1998; 98US-0085696P.

XX PR 21-OCT-1998; 98US-0105234P.

XX PR 27-OCT-1998; 98US-0105877P.

XX PA (CHIR) CHIRON CORP.

XX PA (HYSE-) HYSEQ INC.

XX PI Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
 PI Reinhard C, Giese K, Randazzo F, Kennedy GC, Pot D, Kassam A;
 PI Lamson G, Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
 PI Leshkowitz D, Kita D, Garcia V, Jones LW, Stache-Grain B;

XX DR WPI; 2000-126369/11.

XX PT Polynucleotide library used to determine cancerous states of mammalian
 PT cells.

XX PS Claim 1; Page 616-617; 1097pp; English.

XX CC AAA000010 to AAA02716 represent polynucleotides isolated from cDNA
 CC libraries constructed from human colon cancer cell lines. The present
 CC invention also describes a method of detecting differentially expressed
 CC genes correlated with a cancerous state of a mammalian cell, comprising
 CC detecting at least one differentially expressed gene product in a test
 CC sample derived from a cell suspected of being cancerous, where detection
 CC of the differentially expressed gene product is correlated with a
 CC cancerous state of the cell from which the test sample was derived. The
 CC polynucleotide sequences can be used in a method for detecting
 CC differentially expressed genes correlated with a cancerous state of a
 CC mammalian cell. The polynucleotides can also be used as probes for
 CC detecting and mapping related genes. They can be used in diagnosis and
 CC prognosis of diseases and disorders (e.g. identification of pre-
 CC metastatic or metastatic cancerous states, stages of cancer, or
 CC responsiveness of cancer to therapy). This is particularly for breast
 CC cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
 CC negative breast cancer, lung cancer, and colon cancer

XX SQ Sequence 779 BP; 183 A; 215 C; 186 G; 184 T; 0 U; 11 Other;

Query Match 79.0%; Score 15.8; DB 3; Length 779;
 Best Local Similarity 89.5%; Pred. No. 5.3e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGTCTCTGAGTAGCAG 20
 |||||
 Db 341 GGGCGTCTCGGAGTAGGAG 323
 |||||

RESULT 43
 ABD12260/c
 ID ABD12260 standard; DNA; 882 BP.
 XX
 AC ABD12260;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Pseudomonas aeruginosa polynucleotide #10864.
 XX
 KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
 KW antibacterial.
 XX
 OS Pseudomonas aeruginosa.
 XX
 PN US6551795-B1.
 XX
 PD 22-APR-2003.
 XX
 PF 18-FEB-1999; 99US-00252991.
 XX
 PR 18-FEB-1998; 98US-0074788P.
 PR 27-JUL-1998; 98US-0094190P.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 XX
 PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
 XX WPI; 2003-615309/58.
 DR P-PSDB; ABO78689.
 XX
 PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of
 PT pathological conditions resulting from bacterial infection.
 XX
 PS Disclosure; SEQ ID NO 10864; 455pp; English.
 XX
 CC The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biochip technology. Sequences ABD01397-
 CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 882 BP; 208 A; 299 C; 231 G; 144 T; 0 U; 0 Other;

Query Match 79.0%; Score 15.8; DB 11; Length 882;
 Best Local Similarity 89.5%; Pred. No. 5.4e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGTCTCTGAGTAGCAG 20
 |||||
 Db 177 GGGCGTCTCGGAGTAGCAG 159
 |||||

RESULT 44

ABD12216
 ID ABD12216 standard; DNA; 1203 BP.
 XX
 AC ABD12216;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Pseudomonas aeruginosa polynucleotide #10820.
 XX
 KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
 KW antibacterial.
 XX
 OS Pseudomonas aeruginosa.
 XX
 PN US6551795-B1.
 XX
 PD 22-APR-2003.
 XX
 PF 18-FEB-1999; 99US-00252991.
 XX
 PR 18-FEB-1998; 98US-0074788P.
 PR 27-JUL-1998; 98US-0094190P.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 XX
 PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
 XX WPI; 2003-615309/58.
 DR P-PSDB; ABO78645.
 XX
 PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of
 PT pathological conditions resulting from bacterial infection.
 XX
 PS Disclosure; SEQ ID NO 10820; 455pp; English.
 XX
 CC The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biochip technology. Sequences ABD01397-
 CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 1203 BP; 210 A; 320 C; 396 G; 277 T; 0 U; 0 Other;

Query Match 79.0%; Score 15.8; DB 11; Length 1203;
 Best Local Similarity 89.5%; Pred. No. 5.6e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGTCTCTGAGTAGCAG 20
 |||||
 Db 760 GGGCGTCTCGGAGTAGCAG 778
 |||||

RESULT 45
 ABD07772
 ID ABD07772 standard; cDNA; 2069 BP.
 XX
 AC ABD07772;
 XX
 DT 04-NOV-2004 (first entry)
 XX
 DE Full length human cDNA useful for treating neurological disease Seq 1278.

XX gene; ss; human; oligo-capping method; diagnostic marker; gene therapy;
 KW osteoporosis; neurological disease; Alzheimer's disease;
 KW Parkinson's disease; dementia; short memory; cancer;
 KW sense or motor function; emotional reaction; fear response; panic;
 KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
 KW tranquiliser.
 XX
 OS Homo sapiens.
 XX
 PN EP1447413-A2.
 XX
 PD 18-AUG-2004.
 XX
 PF 12-FEB-2004; 2004EP-000031145.
 XX
 PR 14-FEB-2003; 2003JP-00102207.
 XX
 PR 09-MAY-2003; 2003JP-00131452.
 XX
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 PI Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;
 PI Wakamatsu A, Ishii S, Nagai K, Irie R;
 XX
 DR WPI: 2004-583265/57.
 DR P-PSDB; ADR09728.
 XX
 PT New 1995 cDNA, useful for treating osteoporosis, neurological diseases,
 PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
 XX
 PS Claim 1; SEQ ID NO 1278; 2686pp; English.
 XX
 CC This invention relates to novel, isolated full length human cDNA
 CC molecules and the encoded proteins thereof. Specifically, it refers to
 CC cDNA clones obtained by an oligo-capping method, where none of these
 CC clones are identical to any known human mRNAs. The present invention
 CC describes an immunoassay to identify agonists and antagonists, as well as
 CC antibodies, antisense molecules and siRNAs that can all be used to bind
 CC to and modulate expression of the cDNA molecules. As such, these
 CC molecules are useful for diagnostic markers or therapeutic targets for
 CC the various diseases or morbid states. In particular, they are useful in
 CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's
 CC disease, Parkinson's disease, dementia, short memory and various cancers,
 CC as well as for maintaining equilibrium of sense or motor function, and
 CC for treating emotional reaction, fear response and panic. Accordingly,
 CC they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,
 CC cytostatic and tranquiliser activities. This polynucleotide is a full
 CC length human cDNA sequence of the invention. NOTE: This sequence is not
 CC given in the sequence listing of the specification but can be obtained on
 CC CD-ROM from the European Patent Office, Vienna Sub-office.
 XX
 SQ Sequence 2069 BP; 498 A; 540 C; 586 G; 445 T; 0 U; 0 Other;
 Query Match 79.0%; Score 15.8; DB 13; Length 2069;
 Best Local Similarity 89.5%; Pred. No. 5.9e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 GGGCGTCTCTGAGTAGCAG 20
 DB 573 GGGCGTTTCTGAGGAGCAG 591
 RESULT 46
 AAV48219/c
 ID AAV48219 standard; DNA; 2614 BP.
 XX
 AC AAV48219;
 XX
 DT 09-NOV-1998 (first entry)
 XX
 DE Mouse striated muscle preferentially expressed gene.
 XX
 KW ds; human; striated muscle preferentially expressed protein;

KW smooth muscle; cell proliferation; developmental stage; gamma-interferon;
 KW tissue plasminogen activator; p21 cell cycle; nitric oxide synthetase.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 CDS 1..1803
 FT /*tag= a
 FT /product= "Striated muscle preferentially expressed
 FT protein"
 FT /note= "No stop codon given in protein, however stop
 FT codon present at position 1807. .1809"
 XX
 PN W09835040-A2.
 XX
 PD 13-AUG-1998.
 XX
 PF 06-FEB-1998; 98WO-US002441.
 XX
 PR 06-FEB-1997; 97US-00795868.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Lee M, Hsieh C;
 XX
 DR WPI: 1998-447237/38.
 DR P-PSDB; AAW77049.
 XX
 PT Novel human, rat or mouse aorta or striated-muscle preferentially
 PT expressed proteins - useful for treating e.g. atherosclerosis.
 XX
 PS Claim 18; Fig 22; 88pp; English.
 XX
 CC The striated muscle preferentially expressed protein (SPEG) can be linked
 CC to an enhancer/promoter derived from an aortic preferentially expressed
 CC gene to regulate smooth muscle cell-specific expression. This can be used
 CC as a method of inhibiting vascular smooth muscle cell proliferation. The
 CC nucleic acids are used to direct developmental stage-specific expression
 CC of a heterologous polypeptide which is especially selected from tissue
 CC plasminogen activator (tPA), p21 cell cycle inhibitor, nitric oxide
 CC synthetase, gamma-interferon, atrial natriuretic proteins. These are used
 CC to inhibit the proliferation of smooth muscle cells, e.g. for the
 CC treatment of atherosclerosis
 XX
 SQ Sequence 2614 BP; 540 A; 816 C; 811 G; 447 T; 0 U; 0 Other;
 Query Match 79.0%; Score 15.8; DB 2; Length 2614;
 Best Local Similarity 89.5%; Pred. No. 6.1e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 GGGCGTCTCTGAGTAGCAG 20
 DB 1273 GGGCGTCTCTGAGCAGCAG 1255
 RESULT 47
 AAZ51045/c
 ID AAZ51045 standard; cDNA; 2614 BP.
 XX
 AC AAZ51045;
 XX
 DT 05-JUN-2000 (first entry)
 XX
 DE Mouse striated muscle preferentially expressed gene partial cDNA.
 XX
 KW Mouse; striated muscle preferentially expressed gene; SPEG;
 KW aortic-preferentially-expressed gene-1; APEG-1; striated muscle cell;
 KW aorta; smooth muscle cell; antiarteriosclerotic; vasotropic; treatment;
 KW diagnosis; vascular disease; atherosclerosis; restenosis; ss.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers

FT CDS 1..1809
FT /*tag= a
FT /product= "SPEG protein"
FT /partial
XX
PN WO200009689-A2.
XX
PD 24-FEB-2000.
XX
PF 11-MAY-1999; 99WO-US010298.
XX
PR 14-AUG-1998; 98US-00134250.
PR 30-APR-1999; 99US-00303069.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Lee M, Hsieh C;
XX
DR WPI; 2000-224334/19.
DR P-PSDB; AAY70079.
XX
PT New gene useful for treating and diagnosing vascular diseases comprises a
PT single gene encoding aortic-specific and striated-specific muscle cell
PT isoforms.
XX
PS Claim 30; Fig 22; 88pp; English.
XX
CC The present sequence is a partial cDNA encoding mouse striated muscle
CC preferentially expressed gene (SPEG) protein. This protein was detected
CC in striated muscles of skeletal and cardiac tissues. It is one of the two
CC muscle cell protein isoforms encoded by the aortic-preferentially-
CC expressed gene-1 (APEG-1). The other protein isoform is specific to
CC aortic smooth muscle cells designated APEG-1 protein. The present
CC sequence can be used to identify striated muscle cell specific-promoter
CC which may be useful to direct gene expression in striated muscle cells to
CC treat diseases associated with these muscles. APEG-1 gene is useful for
CC treating and diagnosing vascular diseases such as atherosclerosis and
CC restenosis
XX
SQ Sequence 2614 BP; 540 A; 816 C; 811 G; 447 T; 0 U; 0 Other;

Query Match 79.0%; Score 15.8; DB 3; Length 2614;
Best Local Similarity 89.5%; Pred. No. 6.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGTCTCTGAGTAGCAG 20
Db 1273 GGGCGTCTCTGAGTAGCAG 1255

RESULT 48
ADQ97808/c
ID ADQ97808 standard; DNA; 2928 BP.
XX
AC ADQ97808;
XX
DT 07-OCT-2004 (first entry)
XX
DE Mouse cancer associated sequence MR11-001, SEQ ID 785.
XX
KW Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Mouse; ds.
XX
OS Mus musculus.
XX
PN WO2004060304-A2.
XX
PD 22-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US041389.
XX
PR 27-DEC-2002; 2002US-00330773.
XX
PA (SAGR-) SAGRES DISCOVERY INC.

XX Morris DW, Malandro MS;
XX WPI; 2004-543781/52.
XX
PT New isolated cancer associated nucleic acids comprising at least 10
PT contiguous nucleotides, useful for diagnosing, preventing and/or treating
PT cancers such as leukemia and lymphoma.
XX
PS Claim 1; SEQ ID NO 785; 199pp; English.
XX
CC The present invention relates to cancer associated sequences (ADQ97025-
CC ADQ98004). The sequences are useful for the diagnosis, prevention and/or
CC treatment of cancer, such as leukemia and lymphoma. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2928 BP; 679 A; 840 C; 704 G; 685 T; 0 U; 20 Other;

Query Match 79.0%; Score 15.8; DB 12; Length 2928;
Best Local Similarity 89.5%; Pred. No. 6.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGTCTCTGAGTAGCAG 20
Db 579 GGGCGTCTCTGAGTAGCAG 561

RESULT 49
AAS14505/c
ID AAS14505 standard; DNA; 5000 BP.
XX
AC AAS14505;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human GSTT1 deletion point 5' flanking region.
XX
KW Human; ds; GSTT1; Glutathione-S-transferase theta; 5' flanking sequence;
KW skin cancer; GSTT1*0 allele; oxidative stress; genotyping.
XX
OS Homo sapiens.
XX
PN EP1130112-A1.
XX
PD 05-SEP-2001.
XX
PF 24-FEB-2000; 2000EP-00103844.
XX
PR 24-FEB-2000; 2000EP-00103844.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Sprenger R, Schlagenhauser R, Brinkmann U, Kerb R;
XX
DR WPI; 2001-591524/67.
XX
PT PCR assay to detect presence of single allele e.g., glutathione S-
PT transferase thetaaasterisk0 allele, of deletion mutant involves performing
PT PCR with primers derived from sequences upstream and downstream of
PT deletion area.
XX
PS Disclosure; Page 8-9; 24pp; English.
XX
CC The invention relates to a PCR assay for detecting presence of at least a
CC single allele of deletion mutant GSTT1*0 (glutathione S-transferase theta
CC allele) involves performing PCR with two primers, of which one is from
CC the sequence upstream of the deletion area and the other is from the
CC sequence downstream of the deletion area, and checking the corresponding
CC DNA fragment produced in PCR. The method is useful for detecting presence
CC of at least GSTT1*0 allele, for diagnostic testing of individuals to
CC check whether they are susceptible to toxins or resistant to certain

CC therapeutic agents or belonging to risk groups (e.g. UV-mediated skin
 CC damage, skin cancer and cancers associated with oxidative stress. The
 CC method allows the characterisation and mechanism of the GSTT1 deletion
 CC and identifies 18 kb homology regions flanking GSTT1 which are involved
 CC in the deletion event that produced the *0 allele. The method permits the
 CC unambiguous discrimination of all GSTT1 genotypes (*A/A, *0/0 (both
 CC homozygous), *A/0 (heterozygous)). The technique allows the reproducible
 CC simultaneous discrimination of all the genotypes. The three GSTT1
 CC genotypes detected by these procedure correlated highly significant with
 CC enzyme activity in erythrocytes. The trimodular distribution of
 CC phenotypes at high-, intermediate- and null- activity in homo- and
 CC heterozygotes for the *A allele and *0/0 homozygotes, respectively
 CC indicate a gene dose effect. The present sequence is 5kb of genomic
 CC sequence, 5' to the deletion point, from which PCR primers were designed
 CC enabling the three alleles to be discriminated in an assay of the
 CC invention
 XX
 SQ Sequence 5000 BP; 1230 A; 1231 C; 1464 G; 1075 T; 0 U; 0 Other;
 Query Match 79.0%; Score 15.8; DB 4; Length 5000;
 Best Local Similarity 89.5%; Pred. No. 6.5e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 GGGCGTCTCTGAGTAGCAG 20
 DB 3623 GGGCGTCTCTGAGTAGCAG 3605
 AC ADK40991;
 DT 06-MAY-2004 (first entry)
 XX Novel human kinase gene #11.
 XX
 KW cytotatic; immunomodulator; cardiant; neuroprotective; nootropic;
 KW antiparkinsonian; virucide; antibacterial; fungicide; ophthalmological;
 KW analgesic; hypotensive; immunosuppressive; kinase inhibitor; kinase;
 KW cancer; peripheral nervous system; central nervous system;
 KW Alzheimer's disease; Parkinson's disease; multiple sclerosis;
 KW amyotrophic lateral sclerosis; viral infection; prion infection;
 KW ocular disease; migraine; pain; sexual dysfunction; mood disorder;
 KW attention disorder; cognition disorder; hypotension; hypertension;
 KW psychotic disorder; neurological disorder; dyskinesia;
 KW metabolic disorder; organ transplant rejection; enzyme; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2003057841-A2.
 XX
 PD 17-JUL-2003.
 XX
 PF 31-DEC-2002; 2002WO-US041687.
 XX
 PR 31-DEC-2001; 2001US-0343169P.
 XX
 PA (GRIG/) GRIGORIEV I V.
 PA (SUDA/) SUDARSANAM S.
 XX
 PI Grigoriev IV, Sudarsanam S;
 XX WPI; 2003-587115/55.
 DR
 XX New isolated, enriched or purified nucleic acid molecule encoding a
 PT kinase polypeptide, useful for treating cancer, immune-related diseases,
 PT cardiovascular disease, brain or neuronal-associated diseases and
 PT metabolic disorders.
 XX
 PS Claim 33; SEQ ID NO 98; 491pp; English.

CC The invention relates to novel isolated, enriched or purified nucleic acid
 CC molecules encoding a kinase polypeptide. The nucleic acid molecule
 CC comprises a sequence that: (a) encodes a kinase polypeptide; (b) is a
 CC complement of (a); (c) hybridizes under stringent conditions to (a) and
 CC encodes a naturally occurring kinase polypeptide; (d) encodes the
 CC polypeptide in (a), except that it lacks one or more, but not all, of an
 CC N-terminal domain, C-terminal catalytic domain, a spacer region and a C-
 CC terminal domain, a coiled-coil structure region, a catalytic domain, a C-
 CC terminal tail; or (e) is a complement of (d). The nucleic acid molecules,
 CC polypeptides, methods and substance are useful for treating cancers,
 CC immune-related diseases or disorders, cardiovascular disease, brain or
 CC neuronal-associated diseases, and metabolic disorders. The disorders are
 CC preferably cancers of the tissues or of hematopoietic origin, diseases of
 CC the central or peripheral nervous system, Alzheimer's disease,
 CC Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis,
 CC viral infections, infections caused by prions, infections caused by
 CC bacteria, infections caused by fungi, ocular diseases, migraines, pain,
 CC sexual dysfunction, mood disorders, attention disorders, cognition
 CC disorders, hypotension, hypertension, psychotic disorders, neurological
 CC disorders, dyskinesias, metabolic disorders and organ transplant
 CC rejection. This sequence corresponds to the DNA encoding one of the
 CC kinase polypeptides of the invention.
 XX

SQ Sequence 5727 BP; 1464 A; 1397 C; 1637 G; 1229 T; 0 U; 0 Other;

Query Match 79.0%; Score 15.8; DB 10; Length 5727;
 Best Local Similarity 89.5%; Pred. No. 6.6e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGTCTCTGAGTAGCAG 20

DB 3911 GGGCGTCTCTGAGTAGGAG 3893
 |||||
 |||||

Search completed: March 14, 2005, 20:46:06
 Job time : 294 secs

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OM nucleic - nucleic search, using sw model

Run on: March 14, 2005, 17:14:07 ; Search time 1891 Seconds
(without alignments)
402.583 Million cell updates/sec

Title: US-10-672-399-10

Perfect score: 20

Sequence: 1 agggcgctctgtagtagcag 20

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gsa1:*

9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	100.0	232	6	CB266804
C 2	20	100.0	551	4	BG707429
C 3	20	100.0	551	4	BG707608
C 4	20	100.0	610	5	BX327795
C 5	20	100.0	739	9	AY421570 Pan trogl
C 6	20	100.0	782	4	BI753116
C 7	20	100.0	896	5	BX371636 BX371636
C 8	20	100.0	1084	4	BM544718 AGENCOURT
C 9	20	100.0	1728	9	AY421569
C 10	20	100.0	2072	3	CR602106
C 11	18	90.0	1087	1	AL571167
C 12	17.4	87.0	385	8	BH235764 ATZKC34TF
C 13	17.4	87.0	521	8	AZ408342 LM0179D01
C 14	17.4	87.0	578	7	CO708502
C 15	17.4	87.0	593	8	BH236262
C 16	17.4	87.0	687	9	CE013803
C 17	17.4	87.0	1746	9	AY421571 Mus muscu
C 18	16.8	84.0	210	8	AZ850382 ZM0152P11
C 19	16.8	84.0	249	9	CR037148
C 20	16.8	84.0	252	9	CE277790
C 21	16.8	84.0	402	7	CR012636
C 22	16.8	84.0	464	7	R23689
C 23	16.8	84.0	519	8	AQ229055 HS_2019_A
C 24	16.8	84.0	547	9	CR265831 Reverse's

C 25	16.8	84.0	550	9	CE015183
C 26	16.8	84.0	551	7	CV458871 aof02-9ms
C 27	16.8	84.0	554	4	BI788920 iea1c05.Y
C 28	16.8	84.0	565	6	CA248736 SCSBFL110
C 29	16.8	84.0	569	4	BM333590 MEST179-D
C 30	16.8	84.0	593	9	CG985592 CH240.155
C 31	16.8	84.0	645	8	BH646059 BOH2N67TF
C 32	16.8	84.0	647	8	AZ966847 ZM0237106
C 33	16.8	84.0	664	8	AZ840734 ZM0138122
C 34	16.8	84.0	669	7	CV288705 aof01-9ms
C 35	16.8	84.0	679	9	CR191252 Reverse's
C 36	16.8	84.0	684	1	AV370109
C 37	16.8	84.0	702	9	AG119191 Pan trogl
C 38	16.8	84.0	708	7	CV289631 aof01-8ms
C 39	16.8	84.0	723	7	CV289106 aof01-1ms
C 40	16.8	84.0	730	8	BH316461 CH230-40G
C 41	16.8	84.0	736	9	AG383658 Mus muscu
C 42	16.8	84.0	744	9	AG569158 Mus muscu
C 43	16.8	84.0	744	9	CC552929 CH240.438
C 44	16.8	84.0	764	9	BX982971 Forward's
C 45	16.8	84.0	773	9	AG591654 Mus muscu
C 46	16.8	84.0	773	9	CV292304 aof01-11m
C 47	16.8	84.0	796	9	CL662911 PRI0142d
C 48	16.8	84.0	846	7	CV289382 aof01-2ms
C 49	16.8	84.0	855	9	CR802378
C 50	16.8	84.0	874	9	CR194037 Reverse's
C 51	16.8	84.0	876	7	CV291568 aof01-16m
C 52	16.8	84.0	920	7	CV289351 aof01-7ms
C 53	16.8	84.0	962	9	CNS038EA
C 54	16.8	84.0	1035	9	CNS0650H
C 55	16.8	84.0	1407	3	AK033454 Mus muscu
C 56	16.8	84.0	2800	3	AK051660 Mus muscu
C 57	16.8	84.0	2931	3	AK035662 Mus muscu
C 58	16.4	82.0	166	9	CE771307 tigr-gss-
C 59	16.4	82.0	201	2	BF734506 PN2-AN008
C 60	16.4	82.0	272	2	BF907757 IL2-UT007
C 61	16.4	82.0	283	8	AZ492804 IM0327D07
C 62	16.4	82.0	303	2	BF394207 UI-R-CAO-
C 63	16.4	82.0	327	7	TI9249 d03008T Tes
C 64	16.4	82.0	406	6	CB142104 K-EST0195
C 65	16.4	82.0	446	4	BM827484 K-EST0099
C 66	16.4	82.0	474	2	BF393450 UI-R-CAO-
C 67	16.4	82.0	484	2	BF394808 UI-R-CAO-
C 68	16.4	82.0	499	2	AW962815 EST374888
C 69	16.4	82.0	514	9	AG250246 Lotus cor
C 70	16.4	82.0	538	2	BE742897 601574583
C 71	16.4	82.0	545	6	CA741357 wialc.pk0
C 72	16.4	82.0	552	7	CN300697 170004177
C 73	16.4	82.0	554	6	CB131572 K-EST0181
C 74	16.4	82.0	568	4	BI254811 602974057
C 75	16.4	82.0	572	2	BE296203 601177354
C 76	16.4	82.0	581	5	BP366762 BP366762
C 77	16.4	82.0	585	1	AL046149 DKP2P434A
C 78	16.4	82.0	587	6	CA504333 UI-R-FJ0-
C 79	16.4	82.0	587	6	CA504333 UI-R-FJ0-
C 80	16.4	82.0	588	7	CK889521 SGP161545
C 81	16.4	82.0	595	8	AZ828093 ZM0104G24
C 82	16.4	82.0	599	8	AZ710802 RBC1-24-1
C 83	16.4	82.0	607	5	BP245334 BP245334
C 84	16.4	82.0	630	7	CB340372 OJ48e11.Y
C 85	16.4	82.0	643	4	BJ262582 BJ262582
C 86	16.4	82.0	644	7	CN300707 170006001
C 87	16.4	82.0	661	4	BG761400 602718289
C 88	16.4	82.0	671	2	BE779713 601465250
C 89	16.4	82.0	673	4	BM042146 603635783
C 90	16.4	82.0	682	4	BJ257007 BJ257007
C 91	16.4	82.0	689	2	BE273057 601171394
C 92	16.4	82.0	699	7	CN300693 170005999
C 93	16.4	82.0	700	4	BG388020 602412861
C 94	16.4	82.0	707	4	BM006304 603614984
C 95	16.4	82.0	730	6	CB499497 ssaalhc01
C 96	16.4	82.0	740	4	BG281880 602402619
C 97	16.4	82.0	743	1	AI066022 BSBmMFS20

244	15.8	79.0	495	8	BH070793	BH070793	RPCI-24-3	317	15.8	79.0	720	8	A2825641	A2825641	2M0100N21
245	15.8	79.0	499	1	A1129469	QC44D12.x	CE446925	318	15.8	79.0	724	2	BF430769	BF430769	OG04B02T3
246	15.8	79.0	518	8	CA466925	tigr-g88-	CE466925	319	15.8	79.0	725	6	CA259298	CA259298	SCEQRT301
247	15.8	79.0	521	2	BE097188	UI-R-B01-	BE097188	320	15.8	79.0	728	8	A2330907	A2330907	IM0056N05
248	15.8	79.0	524	4	BG789955	aae61b09.	BG789955	321	15.8	79.0	730	7	CK947974	CK947974	4072678 B
249	15.8	79.0	525	1	AA848303	EST191063	AA848303	322	15.8	79.0	730	9	AG390119	AG390119	Mus muscu
250	15.8	79.0	525	1	A1579376	UI-R-Y0-V	A1579376	323	15.8	79.0	733	6	CA505500	CA505500	UI-R-FS1-
251	15.8	79.0	531	8	A2365345	IM0111024	CA2365345	324	15.8	79.0	733	6	BI689926	BI689926	603310760
252	15.8	79.0	535	6	CB148110	K-EST0204	CB148110	325	15.8	79.0	739	9	AG374036	AG374036	Mus muscu
253	15.8	79.0	538	6	CA228994	SCQGPL305	CA228994	326	15.8	79.0	740	5	BQ204580	BQ204580	UI-R-D21-
254	15.8	79.0	543	2	BF403656	UI-R-CA1-	BF403656	327	15.8	79.0	747	6	CF069084	CF069084	EST669805
255	15.8	79.0	544	9	CE504906	tigr-g88-	CE504906	328	15.8	79.0	747	7	CR452535	CR452535	CR452535
256	15.8	79.0	544	9	CL368014	RPCI44_37	CL368014	329	15.8	79.0	748	7	CO396018	CO396018	AGENCOURT
257	15.8	79.0	545	6	CA142717	SCMCR210	CA142717	330	15.8	79.0	749	3	CR714545	CR714545	Tetraodon
258	15.8	79.0	549	2	BF321524	uz62905.Y	BF321524	331	15.8	79.0	751	6	CA919645	CA919645	EST67363
259	15.8	79.0	551	2	BE232818	138051.MA	BE232818	332	15.8	79.0	767	8	A2664038	A2664038	IM0544F01
260	15.8	79.0	567	2	BE755515	209379.NA	BE755515	333	15.8	79.0	772	5	BQ208145	BQ208145	UI-R-EP0-
261	15.8	79.0	570	7	CF137591	UI-HF-BN0	CF137591	334	15.8	79.0	772	9	AG501097	AG501097	Mus muscu
262	15.8	79.0	570	9	CE073212	tigr-g88-	CE073212	335	15.8	79.0	779	6	CA157161	CA157161	SCEQR2302
263	15.8	79.0	572	5	BQ208206	UI-R-EP0-	BQ208206	336	15.8	79.0	780	7	CF872648	CF872648	trIC002XJ
264	15.8	79.0	572	8	BZ894473	Hg13_0123	BZ894473	337	15.8	79.0	781	4	BG911931	BG911931	602809627
265	15.8	79.0	579	6	CD886512	GL18_1021	CD886512	338	15.8	79.0	796	6	CB667673	CB667673	OSJNEd15B
266	15.8	79.0	585	8	BZ561288	pac82-164	BZ561288	339	15.8	79.0	797	6	CB565688	CB565688	OSJNEc11L
267	15.8	79.0	586	2	BF112935	EST440618	BF112935	340	15.8	79.0	797	7	CO811183	CO811183	AGENCOURT
268	15.8	79.0	588	4	BI806570	BM085976	BI806570	341	15.8	79.0	805	8	BZ577010	BZ577010	meH2_5208
269	15.8	79.0	588	4	BM085976	sah33h09.	BM085976	342	15.8	79.0	806	6	CB322408	CB322408	UI-R-DY0-
270	15.8	79.0	589	8	AQ614855	HS_5140.A	AQ614855	343	15.8	79.0	814	8	BZ574508	BZ574508	meH2_3703
271	15.8	79.0	594	5	BQ208213	UI-R-EP0-	BQ208213	344	15.8	79.0	815	4	BI183098	BI183098	UNL-P-FN-
272	15.8	79.0	594	9	CR165714	Reverse8_8	CR165714	345	15.8	79.0	815	8	BZ574646	BZ574646	meH2_3766
273	15.8	79.0	599	7	CO134881	EST829552	CO134881	346	15.8	79.0	821	4	BI182173	BI182173	UNL-P-FN-
274	15.8	79.0	600	5	BQ570796	UI-M-FB0-	BQ570796	347	15.8	79.0	821	6	CB322420	CB322420	UI-R-DY0-
275	15.8	79.0	600	6	CA757620	OE04E12-T	CA757620	348	15.8	79.0	823	6	CB669819	CB669819	OSJNEe02J
276	15.8	79.0	601	1	AU082994	AU082994	AU082994	349	15.8	79.0	830	7	CV139223	CV139223	EST850432
277	15.8	79.0	603	1	AL703709	DKF2p686D	AL703709	350	15.8	79.0	836	7	CN809455	CN809455	EST0801.M
278	15.8	79.0	606	5	BQ211501	UI-R-DY1-	BQ211501	351	15.8	79.0	850	6	CA131389	CA131389	SCBPR107
279	15.8	79.0	611	9	CE309930	tigr-g88-	CE309930	352	15.8	79.0	850	6	CD758183	CD758183	AGENCOURT
280	15.8	79.0	612	4	BI309184	EST330594	BI309184	353	15.8	79.0	850	7	CO235393	CO235393	WS0264.B2
281	15.8	79.0	612	7	CF670348	RTCNTL_49	CF670348	354	15.8	79.0	853	4	BI183135	BI183135	UNL-P-FN-
282	15.8	79.0	614	2	BB658807	BB658807	BB658807	355	15.8	79.0	858	6	CB635977	CB635977	OSIIEb16P
283	15.8	79.0	622	2	BB619137	BB619137	BB619137	356	15.8	79.0	858	7	CK140982	CK140982	AGENCOURT
284	15.8	79.0	622	6	CT7492	C77492	CT7492	357	15.8	79.0	860	5	EX928485	EX928485	EX928485
285	15.8	79.0	624	4	BI088236	602851292	BI088236	358	15.8	79.0	861	9	CG870336	CG870336	ZMMBSC027
286	15.8	79.0	628	6	CA287018	SCSBSD205	CA287018	359	15.8	79.0	862	7	CO213769	CO213769	WS00930.B
287	15.8	79.0	634	8	AZ725179	RPCI-24-7	AZ725179	360	15.8	79.0	863	9	CR103638	CR103638	Reverse8.B
288	15.8	79.0	634	9	CL714494	OR_BBa003	CL714494	361	15.8	79.0	882	5	BU535451	BU535451	AGENCOURT
289	15.8	79.0	641	1	AL133192	HA1787.Hu	AL133192	362	15.8	79.0	884	7	CK770217	CK770217	958358.MA
290	15.8	79.0	642	9	CL342992	RPCI44_27	CL342992	363	15.8	79.0	900	5	BQ644902	BQ644902	AGENCOURT
291	15.8	79.0	648	7	CF670268	RTCNTL_49	CF670268	364	15.8	79.0	907	4	BI252189	BI252189	602952882
292	15.8	79.0	653	6	CA237780	SCACFL502	CA237780	365	15.8	79.0	907	8	CC092538	CC092538	CSU-K34.1
293	15.8	79.0	653	8	AZ107821	RPCI-23-3	AZ107821	366	15.8	79.0	913	5	BQ919821	BQ919821	AGENCOURT
294	15.8	79.0	655	9	CL736005	OR_BBa006	CL736005	367	15.8	79.0	935	5	BU600244	BU600244	AGENCOURT
295	15.8	79.0	657	9	CE665421	tigr-g88-	CE665421	368	15.8	79.0	937	2	BE573380	BE573380	601333046
296	15.8	79.0	658	2	BB638418	BB638418	BB638418	369	15.8	79.0	953	9	CO099103	CO099103	ISBL-3202
297	15.8	79.0	663	4	CG455956	NF070F10P	CG455956	370	15.8	79.0	983	5	BQ652867	BQ652867	AGENCOURT
298	15.8	79.0	664	9	BE455956	602365242	BE455956	371	15.8	79.0	986	4	BG252608	BG252608	602365242
299	15.8	79.0	664	9	CL197328	tigr-g88-	CL197328	372	15.8	79.0	1006	2	BB609618	BB609618	BB609618
300	15.8	79.0	667	6	CA144711	SCSFR2202	CA144711	373	15.8	79.0	1046	9	AG103111	AG103111	Pan trogl
301	15.8	79.0	675	6	CA153474	RPCI-23-2	CA153474	374	15.8	79.0	1059	8	BZ550919	BZ550919	Pac81-60
302	15.8	79.0	675	8	AZ881605	RPCI-23-2	AZ881605	375	15.8	79.0	1060	4	BM551157	BM551157	AGENCOURT
303	15.8	79.0	676	6	CD768857	AGENCOURT	CD768857	376	15.8	79.0	1061	5	BQ943231	BQ943231	AGENCOURT
304	15.8	79.0	676	8	BZ879838	CH240_293	BZ879838	377	15.8	79.0	1075	4	BM549499	BM549499	AGENCOURT
305	15.8	79.0	676	9	AG142184	Pan trogl	AG142184	378	15.8	79.0	1120	3	AX009264	AX009264	AGENCOURT
306	15.8	79.0	681	2	BB125916	BB125916	BB125916	379	15.8	79.0	1131	2	BF688484	BF688484	602185089
307	15.8	79.0	683	6	CA189499	SCCCLR1C0	CA189499	380	15.8	79.0	1170	3	AP116668	AP116668	Homo sapi
308	15.8	79.0	685	4	BJ167394	BJ167394	BJ167394	381	15.8	79.0	1173	8	CC211181	CC211181	CH261-186
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312	15.8	79.0	701	6	CB565689	OSJNEc11L	CB565689	385	15.8	79.0	2348	3	AX031142	AX031142	Mus muscu
313	15.8	79.0	702	3	CR694966	Tetraodon	CR694966	386	15.8	79.0	2363	3	AX033189	AX033189	Mus muscu
314	15.8	79.0	702	7	CK967262	4082587.B	CK967262	387	15.8	79.0	2445	3	AX032530	AX032530	Mus muscu
315	15.8	79.0	709	9	AG566979	Mus muscu	AG566979	388	15.8	79.0	2504	3	AX036778	AX036778	Mus muscu
316	15.8	79.0	712	9	AG336188	Mus muscu	AG336188	389	15.8	79.0	2522	3	BC042506	BC042506	Mus muscu

C 390	15.8	79.0	2549	3	AK041713	Mus muscu
C 391	15.8	79.0	2559	3	AK084516	Mus muscu
C 392	15.8	79.0	2943	3	AK016569	Mus muscu
C 393	15.8	79.0	2999	3	AK087790	Mus muscu
C 394	15.8	79.0	3375	3	AK085739	Mus muscu
C 395	15.8	79.0	3479	3	AK035841	Mus muscu
C 396	15.8	79.0	6616	3	AK090124	Mus muscu
C 397	15.4	77.0	141	1	AV012267	AV012267
C 398	15.4	77.0	279	2	BB358001	BB358001
C 399	15.4	77.0	313	1	AA355948	EST64473
C 400	15.4	77.0	335	2	BF326376	PN3-AN009
C 401	15.4	77.0	344	8	AQ065272	HS 2179_B
C 402	15.4	77.0	347	7	CN955224	2721_52-3
C 403	15.4	77.0	397	6	CA194388	SCRFSB102
C 404	15.4	77.0	406	5	BY227135	BY227135
C 405	15.4	77.0	423	1	AA584698	no09G12.8
C 406	15.4	77.0	442	7	CN956589	4089_5001
C 407	15.4	77.0	445	8	AQ057771	CIT-HSP-2
C 408	15.4	77.0	455	9	CR158349	Reverse 8
C 409	15.4	77.0	462	4	BG471874	602513351
C 410	15.4	77.0	487	1	AT1716236	UI-R-YO-a
C 411	15.4	77.0	489	6	CD122121	MEI-0071P
C 412	15.4	77.0	499	7	CF608675	GERMO01_0
C 413	15.4	77.0	515	8	AQ398204	mgxb0010E
C 414	15.4	77.0	521	6	CD922380	G750_10J2
C 415	15.4	77.0	540	8	AZ097714	RPCI-23-4
C 416	15.4	77.0	572	5	BP227693	BP227693
C 417	15.4	77.0	580	5	BP340000	BP340000
C 418	15.4	77.0	581	5	BP254330	BP254330
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C 420	15.4	77.0	584	8	AZ600021	1M0416108
C 421	15.4	77.0	585	5	BP276512	BP276512
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C 425	15.4	77.0	611	7	CV023475	426_Full1
C 426	15.4	77.0	618	4	BJ298299	BJ298299
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C 442	15.4	77.0	697	2	BE262251	601153069
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C 444	15.4	77.0	721	9	CL384721	RPCI44_32
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C 450	15.4	77.0	760	6	CA489510	AGENCOURT
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C 453	15.4	77.0	786	4	BG685473	602637335
C 454	15.4	77.0	789	4	B1833116	603050832
C 455	15.4	77.0	794	4	B1907560	603065920
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C 457	15.4	77.0	800	5	EX880681	EX880681
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C 465	15.4	77.0	827	2	BE561700	601345766
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C 468	15.4	77.0	862	4	B1261265	602972930
C 469	15.4	77.0	868	4	BG759673	602713366
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C 471	15.4	77.0	875	9	CC607943	OGUKO46TH
C 472	15.4	77.0	883	8	CC349707	OGIAO03TV
C 473	15.4	77.0	886	5	EX365216	EX365216
C 474	15.4	77.0	889	4	B1910959	603069360
C 475	15.4	77.0	893	5	BQ691775	AGENCOURT
C 476	15.4	77.0	894	5	BQ686301	AGENCOURT
C 477	15.4	77.0	895	5	EX355234	EX355234
C 478	15.4	77.0	899	5	B0956373	AGENCOURT
C 479	15.4	77.0	910	4	B1523808	603051919
C 480	15.4	77.0	917	4	B1196513	602755631
C 481	15.4	77.0	917	5	BQ878375	AGENCOURT
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C 483	15.4	77.0	921	5	BQ422117	AGENCOURT
C 484	15.4	77.0	933	4	BG330519	602430195
C 485	15.4	77.0	933	6	BG420889	602451110
C 486	15.4	77.0	937	6	CD250920	AGENCOURT
C 487	15.4	77.0	937	4	BG828993	602753313
C 488	15.4	77.0	946	5	BQ877377	AGENCOURT
C 489	15.4	77.0	947	5	BQ690395	AGENCOURT
C 490	15.4	77.0	950	5	EX325348	EX325348
C 491	15.4	77.0	951	2	BQ642330	AGENCOURT
C 492	15.4	77.0	961	2	BE791780	601582145
C 493	15.4	77.0	965	1	AL560618	AL560618
C 494	15.4	77.0	965	1	B1199260	602758561
C 495	15.4	77.0	967	9	CC607948	OGUKO46TV
C 496	15.4	77.0	968	2	BE735466	601304283
C 497	15.4	77.0	968	9	CR169736	Forward 8
C 498	15.4	77.0	971	7	CN972814	20311_124
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C 500	15.4	77.0	984	5	EX377152	EX377152

ALIGNMENTS

RESULT 1	CB266804/c	232 bp	mRNA	linear	EST 20-FEB-2003
CB266804/c	1005710 Human Fat Cell 5'-Stretch Plus	cdna	Library	Homo sapiens	
LOCUS	CDNA 5', mRNA sequence.				
DEFINITION	CDNA 5', mRNA sequence.				
ACCESSION	CB266804.1	GI:28441390			
VERSION	EST.				
KEYWORDS	CB266804.1				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 232)				
AUTHORS	Yang, R.-Z., Shuldiner, A., and Gong, D.-W.				
TITLE	EST analysis of human adipose gene expression				
JOURNAL	Unpublished (2002)				
COMMENT	Contact: Gong Da-Wei Division of Endocrinology, Diabetes and Nutrition University of Maryland 660 Redwood St., HH497, Baltimore, MD 21201, USA Tel: 410 706 1672 Fax: 410 706 1622 Email: dgong@medicine.umaryland.edu PCR Primers FORWARD: CTCGGAAGCGCGCAATCTGTGTGT BACKWARD: AATACGACTACATAGCGGAATTGG Seq primer: GTTGGTACCGGAATTC. Location/Qualifiers 1..232 /organism="Homo sapiens"				

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/note="Vector: lambdaTriplex"

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
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Db 184 AGGGCGTCTCTGAGTAGCAG 165

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DEFINITION 602672848F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4795643 5',
mRNA sequence.
ACCESSION BG707429
VERSION BG707429.1 GI:13983769
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 551)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10678 row: p column: 12
High quality sequence stop: 551.
Location/Qualifiers
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(gtcgag); Oligo-dT primed using primer
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insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

ORIGIN
Query Match      100.0%; Score 20; DB 4; Length 551;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 470 AGGGCGTCTCTGAGTAGCAG 451

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clone CSOD1027YJ02 5-PRIME, mRNA sequence.
ACCESSION BX327795
VERSION BX327795.2 GI:46277978
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 610)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10678 row: p column: 12
High quality sequence stop: 551.
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(gtcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

ORIGIN
Query Match      100.0%; Score 20; DB 4; Length 551;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
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Db 470 AGGGCGTCTCTGAGTAGCAG 451

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AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On May 2, 2003 this sequence version replaced gi:30340686.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 9502.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?s=CS0BAG028ZH06_CS02640_1&c=9502.r

FEATURES
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 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
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 DEFINITION Genomic survey sequence.
 ACCESSION AY421570
 VERSION AY421570.1 GI:39748429
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 1 (bases 1 to 739)
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
 Adams, M.D. and Cargill, M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 Science 302 (5652), 1960-1963 (2003)
 14671302
 2 (bases 1 to 739)
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
 Adams, M.D. and Cargill, M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
 FEATURES
 source
 Location/Qualifiers
 1..739

AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On May 2, 2003 this sequence version replaced gi:30340686.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 9502.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?s=CS0BAG028ZH06_CS02640_1&c=9502.r

FEATURES
 source
 Location/Qualifiers
 1..782
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5196399"
 /lab_host="DH10B"
 /clone_lib="NIH MGC 114"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site: 1: NotI;
 Site 2: EcoRV (destroyed); RNA source anonymous pool of 6
 male brains, age range 23-27 yo. Library is oligo-dT
 primed and directionally cloned (EcoRV site is destroyed
 upon cloning). Average insert size 1.5 kb, insert size
 range 1-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 019. Note:
 this is a NIH_MGC Library."

ORIGIN
 Query Match 100.0%; Score 20; DB 4; Length 782;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
 ||||||||||||||||||
 Db 433 AGGGCGTCTCTGAGTAGCAG 414

RESULT 7

gene
 /organism="Pan troglodytes"
 /mol_type="Genomic DNA"
 /db_xref="taxon:9598"
 <1..>739
 /gene="HAS1"
 /locus_tag="HCM7601"

ORIGIN
 Query Match 100.0%; Score 20; DB 9; Length 739;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
 ||||||||||||||||||
 Db 354 AGGGCGTCTCTGAGTAGCAG 335

RESULT 6
 BI753116/c 782 bp mRNA linear EST 25-SEP-2001
 LOCUS 603025961F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5196399 5',
 DEFINITION mRNA sequence.
 ACCESSION BI753116
 VERSION BI753116.1 GI:15744694
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 782)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM11491 row: j column: 16
 High quality sequence stop: 780.
 Location/Qualifiers
 1..782
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5196399"
 /lab_host="DH10B"
 /clone_lib="NIH MGC 114"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site: 1: NotI;
 Site 2: EcoRV (destroyed); RNA source anonymous pool of 6
 male brains, age range 23-27 yo. Library is oligo-dT
 primed and directionally cloned (EcoRV site is destroyed
 upon cloning). Average insert size 1.5 kb, insert size
 range 1-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 019. Note:
 this is a NIH_MGC Library."

FEATURES
 source
 Location/Qualifiers
 1..782
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5196399"
 /lab_host="DH10B"
 /clone_lib="NIH MGC 114"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site: 1: NotI;
 Site 2: EcoRV (destroyed); RNA source anonymous pool of 6
 male brains, age range 23-27 yo. Library is oligo-dT
 primed and directionally cloned (EcoRV site is destroyed
 upon cloning). Average insert size 1.5 kb, insert size
 range 1-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 019. Note:
 this is a NIH_MGC Library."

ORIGIN
 Query Match 100.0%; Score 20; DB 4; Length 782;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
 ||||||||||||||||||
 Db 433 AGGGCGTCTCTGAGTAGCAG 414

RESULT 7

BX371636
 LOCUS BX371636 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CSODI027YJ02 3-PRIME, mRNA sequence.
 ACCESSION BX371636
 VERSION BX371636.2 GI:46616231
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 896)
 Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 8, 2003 this sequence version replaced gi:30450029.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: segret@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 9502.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?a=CS0BA1019ZC12_CS01819_1&c=9502.r

FEATURES
 source
 Location/Qualifiers
 1..896
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSODI027YJ02"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
 Query Match 100.0%; Score 20; DB 5; Length 896;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AGGGCGTCTCTGAGTAGCAG 20
 Db 134 AGGGCGTCTCTGAGTAGCAG 153

RESULT 8
 BM544718/c
 LOCUS BM544718 1084 bp mRNA linear EST 20-FEB-2002
 DEFINITION AGENCOURT 6494603 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5727446
 5' mRNA sequence.
 ACCESSION BM544718
 VERSION BM544718.1 GI:18776197
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1084)
 NIH-MGC http://mgc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Invitrogen
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)

DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNL at:
 http://image.llnl.gov
 Plate: LLAM12721 row: i column: 15
 High quality sequence start: 5
 High quality sequence stop: 689.
 Location/Qualifiers
 1..1084
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5727446"
 /tissue_type="hippocampus"
 /lab_host="DH10B"
 /clone_lib="NIH MGC 124"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: EcoRV
 (destroyed); Site 2: NotI; RNA source male hippocampus,
 age 27. Library is oligo-dT primed and directionally
 cloned (EcoRV site is destroyed upon cloning). Average
 insert size 1.4 kb, insert size range 0.9-4 kb. Library is
 normalized and enriched for full-length clones and was
 constructed by C. Gruber (Invitrogen). Research Genetics
 tracking code 012."

ORIGIN
 Query Match 100.0%; Score 20; DB 4; Length 1084;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AGGGCGTCTCTGAGTAGCAG 20
 Db 498 AGGGCGTCTCTGAGTAGCAG 479

RESULT 9
 AY421569/c
 LOCUS AY421569 1728 bp DNA linear GSS 17-DEC-2003
 DEFINITION Homo sapiens HAS1 gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 ACCESSION AY421569
 VERSION AY421569.1 GI:39748428
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1728)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
 Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 Science 302 (5652), 1960-1963 (2003)
 14671302
 2 (bases 1 to 1728)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
 Adams,M.D. and Cargill,M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
 Location/Qualifiers
 1..1728
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 <1..>1728
 /gene="HAS1"


```

/db_xref="taxon:3702"
/clone="ATZKC34"
/clone_lib="ATZK"
/note="Vector: pHO2; Site 1: BatXI; 2-3 kb sheared BAC
DNA inserted into pHO2 using BatXI linkers"

ORIGIN
Query Match      87.0%; Score 17.4; DB 8; Length 385;
Best Local Similarity 94.7%; Pred. No. 8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGCGTCTCTGAGTAGCAG 20
    |||||
Db 101 GGGCTTCTCTGAGTAGCAG 83

RESULT 13
AZ408342/c
LOCUS
DEFINITION
IM0179D01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0179D01 R, genomic survey sequence.
ACCESSION
AZ408342
VERSION
AZ408342.1 GI:10532355
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 521)
Dunn,D., Aoyagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: rdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0179 row: D column: 01
Seq primer: CACAGGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 521.
Location/Qualifiers
1..521
/organism="Mus musculus"
/mol_type="genomic DNA"
/strains="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0179D01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnases/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match      87.0%; Score 17.4; DB 8; Length 521;
Best Local Similarity 94.7%; Pred. No. 8.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCA 19
    |||||
Db 76 AGGGCGTCTCCGAGTAGCA 58

RESULT 14
CO708502
LOCUS
DEFINITION
DG14-10b23 DG14-muscle Canis familiaris cDNA 3', mRNA sequence.
ACCESSION
CO708502
VERSION
CO708502.1 GI:50673643
KEYWORDS
EST.
SOURCE
Canis familiaris (dog)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 578)
Schlueter,T., Hermanns,J., Weindel,M., Schuette,D., Kranz,H.,
Henrich,J. and Loebbert,R.
Dog arrayTAG cDNA clone collection
Unpublished (2004)
Contact: Thomas Schlueter
LION bioscience AG
Walhoferstrasse 98, D-69123 Heidelberg, Germany
Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
Email: Thomas.Schlueter@lionbioscience.com.
Location/Qualifiers
1..578
/organism="Canis familiaris"
/mol_type="mRNA"
/strain="Beagle"
/db_xref="taxon:9615"
/tissue_type="muscle"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="DG14-muscle"
/note="Organ: muscle; Vector: Dog pBluescript LION"

ORIGIN
Query Match      87.0%; Score 17.4; DB 7; Length 578;
Best Local Similarity 94.7%; Pred. No. 8.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGCGTCTCTGAGTAGCAG 20
    |||||
Db 487 GGGCGTCTCTGAGTAGGAG 505

RESULT 15
BH236262/c
LOCUS
DEFINITION
ATZKE45TF ATZK Arabidopsis thaliana genomic clone ATZKE45, genomic
survey sequence.
ACCESSION
BH236262
VERSION
BH236262.1 GI:16906620
KEYWORDS
GSS.
SOURCE
Arabidopsis thaliana (chale crese)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

```


Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 210)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0152 row: P column: 11
Seq primer: CTTGTAAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 210.

FEATURES source
Location/Qualifiers
1..210
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0152P11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_libs="Mouse 10kb plasmid UUCG1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 84.0%; Score 16.8; DB 8; Length 210;
Best Local Similarity 90.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
||||| ||||| ||||| ||||| |||||
Db 82 AGGGCGTCTCTGAGTAGCAG 101

RESULT 19

LOCUS CR037148 249 bp DNA linear GSS 05-JUL-2004

DEFINITION Forward strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN307118, genomic survey sequence.

ACCESSION CR037148

VERSION CR037148.1 GI:4970203

KEYWORDS GSS; genome survey sequence; MICR.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 249)

AUTHORS Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J. and Bradley, A.

TITLE Direct Submission

JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICR

FEATURES source
Location/Qualifiers
1..249
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN307118"
/clone_lib="MHPN"

ORIGIN

Query Match 84.0%; Score 16.8; DB 9; Length 249;
Best Local Similarity 90.0%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
||||| ||||| ||||| ||||| |||||
Db 187 AGGGAGTCTCTGAGTAGCAG 168

RESULT 20

LOCUS CE277790/c 252 bp DNA linear GSS 26-SEP-2003

DEFINITION tigr-gss-dog-17000333680929 Dog Library Canis familiaris genomic, genomic survey sequence.

ACCESSION CE277790

VERSION CE277790.1 GI:36025605

KEYWORDS GSS

SOURCE Canis familiaris (dog)

ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (bases 1 to 252)

AUTHORS Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.

TITLE The dog genome: survey sequencing and comparative analysis

JOURNAL Science 301 (5641), 1898-1903 (2003)

MEDLINE 22875432

PUBMED 14512627

COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.

FEATURES source
Location/Qualifiers
1..252
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_libs="Dog Library"
/note="Site 1: BetXI; Libraries were prepared from peripheral blood"

ORIGIN

Query Match 84.0%; Score 16.8; DB 9; Length 252;
Best Local Similarity 90.0%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
||||| ||||| ||||| ||||| |||||
Db 56 AGGGCGTCTCTGAGTAGCAG 37

```

RESULT 21
CR012636/c
LOCUS
DEFINITION
  CR012636 402 bp DNA linear GSS 05-JUL-2004
  Reverse strand read from insert in 3'HPRT insertion targeting and
  chromosome engineering clone MHPP341k19, genomic survey sequence.
ACCESSION
  CR012636.1 GI:49745683
VERSION
  GSS; Genome survey sequence; MICER.
KEYWORDS
  Mus musculus (house mouse)
SOURCE
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 402)
REFERENCE
  Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
  Jokers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
  Rogers,J. and Bradley,A.
  Direct Submision
JOURNAL
  Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
  CB10 1SA, UK. http://www.sanger.ac.uk/MICER
FEATURES
  source
    1..402
    Location/Qualifiers
      /organism="Mus musculus"
      /mol_type="genomic DNA"
      /db_xref="taxon:10090"
      /clone="MHPP341k19"
      /clone_lib="MHPP"

ORIGIN
  Query Match 84.0%; Score 16.8; DB 9; Length 402;
  Best Local Similarity 90.0%; Pred. No. 1.6e+03;
  Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
    ||||| ||||| ||||| |||||
Db 317 AGGGATCTCTGAGTAGCAG 298

RESULT 22
R23689/c
LOCUS
DEFINITION
  YQ32h10.r1 Soares infant brain IN1B Homo sapiens cDNA clone
  IMAGE:34208 5', mRNA sequence.
ACCESSION
  R23689.1 GI:778577
VERSION
  EST.
KEYWORDS
  Homo sapiens (human)
SOURCE
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 464)
REFERENCE
  Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
  Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
  Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,P.,
  Trevisakis,E., Waterston,R., Williamson,A., Wohldmann,P. and
  Wilson,R.
  The WashU-Merck EST Project
JOURNAL
  Unpublished (1995)
COMMENT
  Contact: Wilton RK
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: est@watson.wustl.edu
  Insert Size: 1583
  High quality sequence stops: 298 Source: IMAGE Consortium, LLNL
  This clone is available royalty-free through LLNL; contact the
  IMAGE Consortium (info@image.llnl.gov) for further information.
  Insert Length: 1583 Std Error: 0.00
  Seq primer: M13RP1
  High quality sequence stop: 298.
  Location/Qualifiers
    1..464

FEATURES
  source
    Location/Qualifiers
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="GDB:406555"
      /db_xref="taxon:9606"
      /clone="IMAGE:34208"
      /sex="female"
      /dev_stage="73 days post natal"
      /lab_host="DH10B (ampicillin resistant)"
      /clone_lib="Soares infant brain IN1B"
      /note="Organ: whole brain; Vector: Lafmid BA; Site 1: Not
      I; Site 2: Hind III; 1st strand cDNA was primed with a Not
      I - oligo(GT) primer [5',
      AACTGGAGAATTCGGCCGCGAGGATTTTTTTTTTTT 3'];
      double-stranded cDNA was ligated to Hind III adaptors
      (Pharmacia), digested with Not I and directionally cloned
      into the Not I and Hind III sites of the Lafmid BA vector.
      Library went through one round of normalization. Library
      constructed by Bento Soares and M.Fatima Bonaldo."
```

```

Query Match      84.0%; Score 16.8; DB 8; Length 519;
Best Local Similarity 90.0%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
    ||||| ||||| ||||| |||||
Db 283 AGGCATCTCTGAGTTGCAG 302

RESULT 24
CR265831/c
LOCUS
DEFINITION Reverse strand read from insert in 5'HPRT insertion targeting and
             chromosome engineering clone MHPN303b23, genomic survey sequence.
ACCESSION CR265831
VERSION 1
KEYWORDS GSS; genome survey sequence; MICER.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 547)
AUTHORS Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
Rogers,J. and Bradley,A.
TITLE Direct Submision
JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgehire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICER
FEATURES
    source
        Location/Qualifiers
            1..547
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /db_xref="taxon:10090"
            /clone="MHPN303b23"
            /clone_lib="MHPN"

ORIGIN
Query Match      84.0%; Score 16.8; DB 9; Length 547;
Best Local Similarity 90.0%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
    ||||| ||||| ||||| |||||
Db 540 AGGAGTCACTGAGTAGCAG 521

RESULT 25
CE015183/c
LOCUS
DEFINITION tigr-gss-dog-17000321305524 Dog Library Canis familiaris genomic,
             genomic survey sequence.
ACCESSION CE015183
VERSION 1
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris

REFERENCE 1 (bases 1 to 550)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208

Query Match      84.0%; Score 16.8; DB 9; Length 550;
Best Local Similarity 90.0%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
    ||||| ||||| ||||| |||||
Db 217 AGGAGTCTCAGAGTAGCAG 198

RESULT 26
CV458871/c
LOCUS
DEFINITION aof02-9ms4-f04 Aof02 Asparagus officinalis cDNA clone
ACCESSION CV458871
VERSION 1
KEYWORDS EST.
SOURCE Asparagus officinalis (garden asparagus)
ORGANISM Asparagus officinalis

REFERENCE 1 (bases 1 to 551)
AUTHORS dePamphilis,C., Carlson,J., Ma,H., Soltis,D., Soltis,P.,
Oppenheimer,D., Frohlich,M., Doyle,J., Tankalev,S., Webb,M.,
Leebens-Mack,J., Landherr,L., Ilut,D. and Wall,K.
TITLE Generation of ESTs from early female inflorescences of Asparagus
officinalis
JOURNAL Unpublished (2004)
COMMENT Contact: Claude dePamphilis or James Leebens-Mack
Mueller Laboratory
Penn State University
208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn
State University, University Park, PA 16802, USA
Tel: 814 863 6413
Fax: 814 865 9131
Email: cwd3@psu.edu or jhl10@psu.edu
The sequence provided is trimmed of vector and low quality regions.
Full sequence and original trace file are available from the Plant
Genome Network website (http://pgn.cornell.edu)
Plate: aof02-9ms4 row: f column: 04
Seq primer: M13F.

FEATURES
    source
        Location/Qualifiers
            1..551
            /organism="Asparagus officinalis"
            /mol_type="mRNA"
            /db_xref="taxon:4686"
            /clone="aof02-9ms4-f04"
            /tissue type="female inflorescences"
            /lab host="SOLR"
            /clone_lib="Aof02"
            /note="Vector: pBluescript SK (+/-); Site.1: EcoRI;
            Site.2: XhoI; This is a directionally cloned,
            non-normalized library. This library has been generated by
            the Floral Genome Project (FGP). The Floral Genome Project
            is funded by NSF's Plant Genome Research Program
            (DBI-0115684). More information about the project can be
            obtained at http://fgp.bio.psu.edu"

```

```

Email: ekirknes@tigr.org
Class: shotgun.
Location/Qualifiers
    1..550
    /organism="Canis familiaris"
    /mol_type="genomic DNA"
    /strains="Standard Poodle"
    /db_xref="taxon:9615"
    /clone_lib="Dog Library"
    /note="Site 1: BstXI; Libraries were prepared from
    peripheral blood"

FEATURES
    source
        Location/Qualifiers
            1..550
            /organism="Canis familiaris"
            /mol_type="genomic DNA"
            /strains="Standard Poodle"
            /db_xref="taxon:9615"
            /clone_lib="Dog Library"
            /note="Site 1: BstXI; Libraries were prepared from
            peripheral blood"

ORIGIN
Query Match      84.0%; Score 16.8; DB 9; Length 550;
Best Local Similarity 90.0%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
    ||||| ||||| ||||| |||||
Db 217 AGGAGTCTCAGAGTAGCAG 198

RESULT 26
CV458871/c
LOCUS
DEFINITION aof02-9ms4-f04 Aof02 Asparagus officinalis cDNA clone
ACCESSION CV458871
VERSION 1
KEYWORDS EST.
SOURCE Asparagus officinalis (garden asparagus)
ORGANISM Asparagus officinalis

REFERENCE 1 (bases 1 to 551)
AUTHORS dePamphilis,C., Carlson,J., Ma,H., Soltis,D., Soltis,P.,
Oppenheimer,D., Frohlich,M., Doyle,J., Tankalev,S., Webb,M.,
Leebens-Mack,J., Landherr,L., Ilut,D. and Wall,K.
TITLE Generation of ESTs from early female inflorescences of Asparagus
officinalis
JOURNAL Unpublished (2004)
COMMENT Contact: Claude dePamphilis or James Leebens-Mack
Mueller Laboratory
Penn State University
208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn
State University, University Park, PA 16802, USA
Tel: 814 863 6413
Fax: 814 865 9131
Email: cwd3@psu.edu or jhl10@psu.edu
The sequence provided is trimmed of vector and low quality regions.
Full sequence and original trace file are available from the Plant
Genome Network website (http://pgn.cornell.edu)
Plate: aof02-9ms4 row: f column: 04
Seq primer: M13F.

FEATURES
    source
        Location/Qualifiers
            1..551
            /organism="Asparagus officinalis"
            /mol_type="mRNA"
            /db_xref="taxon:4686"
            /clone="aof02-9ms4-f04"
            /tissue type="female inflorescences"
            /lab host="SOLR"
            /clone_lib="Aof02"
            /note="Vector: pBluescript SK (+/-); Site.1: EcoRI;
            Site.2: XhoI; This is a directionally cloned,
            non-normalized library. This library has been generated by
            the Floral Genome Project (FGP). The Floral Genome Project
            is funded by NSF's Plant Genome Research Program
            (DBI-0115684). More information about the project can be
            obtained at http://fgp.bio.psu.edu"

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ORIGIN

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Query Match      84.0%; Score 16.8; DB 7; Length 551;
Best Local Similarity 90.0%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
    ||||| ||||| ||||| |||||
Db 161 AGGGCGTCTCAGAGTGCGAG 142

RESULT 27
LOCUS BI788920
DEFINITION ie41c05.v1 Kaestner ngn3 wt Mus musculus cDNA 5', mRNA linear EST 01-OCT-2001
ACCESSION BI788920
VERSION BI788920.1 GI:15816645
SOURCE EST.
ORGANISM Mus musculus (house mouse)
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 554)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marx, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R.,
Williams, T., Jackson, F. and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: ie41c05.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Pancreas was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,
2000) Library was constructed by Catherine Lee DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Marie Searce
(msearce@mail.med.upenn.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 434.

FEATURES
source
1..554
    /organism="Mus musculus"
    /mol_type="mRNA"
    /accession="U129/Sv x CD1"
    /db_xref="taxon:10090"
    /dev_stage="p.c. 14.5"
    /lab_host="E. coli-DH12S (GIBCO)"
    /clone_lib="Kaestner ngn3 wt"
    /note="Organ: pancreas; Vector: pSPORT1 (GIBCO); Site_1:
    Not 1; Site_2: Sal I; The library was prepared by
    Catherine S. Lee and has not been published. The pancreas
    was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,
    2000). The cDNA's were prepared with an oligo containing a
    NotI site, and SalI linkers were added to the ends. The
    inserts were cut with NotI before being cloned into the
    NotI-SalI sites in the vectors. This is one of two
    libraries, ngn3 wt and ngn3 -/- . The wt library is in
    pSPORT1, T7 promoter is 5'."

Query Match      84.0%; Score 16.8; DB 4; Length 554;
Best Local Similarity 90.0%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
    ||||| ||||| ||||| |||||
Db 70 AGGGTTCTCTGAGTAGCAG 89

RESULT 28
LOCUS CA248736
DEFINITION CA248736
ACCESSION CA248736
VERSION CA248736.1 GI:35330676
SOURCE EST.
ORGANISM Saccharum officinarum
REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.
1 (bases 1 to 565)
Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: patricia@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 104 row: B column: 09
Seq primer: T7 Promoter Primer.
Location/Qualifiers
1..565
    /organism="Saccharum officinarum"
    /mol_type="mRNA"
    /db_xref="taxon:4547"
    /clone="SCSBFL1104B09"
    /lab_host="DH10B"
    /note="Organ: Inflorescence at beginning of development
    (1cm-long); Vector: pSPORT1; Site_1: SalI; Site_2: NotI;
    An unidirectional cDNA library generated from
    Inflorescence at beginning of development (1cm-long)).
    cDNA was prepared at beginning of development using Superscript
    Plasmid System Kit (Invitrogen). The double-strand cDNAs
    were fractionated in a sepharose CL-2B 40cm-columns and
    fragments sizing between 0.8 and 1.5 Kb were
    directionally cloned into the vector. Details of each
    source of RNA and library construction can be obtained at
    http://sucst.lad.ic.unicamp.br/public"

Query Match      84.0%; Score 16.8; DB 6; Length 565;
Best Local Similarity 90.0%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
    ||||| ||||| ||||| |||||
Db 10 AGGGCGTCTCGGAGGAGCAG 29

RESULT 29
LOCUS BM335950/c
DEFINITION BM335950
ACCESSION BM335950
VERSION BM335950.1 GI:18166111
SOURCE EST.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Query Match      84.0%; Score 16.8; DB 4; Length 554;
Best Local Similarity 90.0%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
    ||||| ||||| ||||| |||||
Db 70 AGGGTTCTCTGAGTAGCAG 89

```

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 569)

Wen.T.J., Qiu.F., Guo.L., Aehlock.D.A and Schnable.P.S

Expressed Sequence Tags from B73 Maize: various stages and tissues

Including seedlings treated with a variety of hormones

Unpublished (2001)

Contact: Patrick S. Schnable

Schnable Laboratory

Iowa State University

G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA

Tel: 515-294-0975

Fax: 515-294-2299

Email: schnable@iastate.edu

Individual basecall and confidence value were assigned using the

Phred software,

(<http://depts.washington.edu/ventures/collabtr/direct/index.htm#b>

rt). Overall sequence quality assessment and vector trimming were

conducted using the Lucy software (<http://www.tigr.org/softlab/lucy>).

Lucy parameters were set to ensure an overall trimmed quality of

97.5% or better without any vector fragments in the chosen

high-quality region of each sequence. Low-quality bases between the

poly-T and the high-quality region were replaced with N's to serve

as spacers.

PCR Primers

FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)

BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)

Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).

FEATURES

source

1..569
 Location/Qualifiers
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="B73"
 /db_xref="taxon:4577"
 /clone="MEST179-D02"
 /tissue_type="mixed"
 /lab_host="DH10B"
 /clone_lib="ISUM5-RN"
 /note="Vector: pT7T3PAC; Site 1: EcoRI; Site 2: NotI;

Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG), Mixed mature tissues (17, 21, 38, 69, 77 DAG), Kernels (3, 5, 10, 15, 20, 25, 30, DAP), Adventitious roots (65 DAG), Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0.2-3.0 cm, 53, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated first ear, ear shank, etiolated seedlings, callus, Cycloheximide-treated callus, Anaerobic treated seedlings, NAA (a-Naphthalene acetic acid)-treated seedlings, Kinetin-treated seedlings, ACPG (1-aminocyclopropane-1-carboxylic acid)-treated seedlings, Brassinolide-treated seedlings, ABA (Abscisis acid)-treated seedlings, GA (Gibberellic acid)-treated seedlings, JA (Jasmonic acid)-treated seedlings. ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT primer (5' NAACTGGAAGATTCGGCGCGAGGAATTTTTTTTTTTTTT). The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT7T3PAC vector. The library then went through one round of normalization to Cot value of 5 based on the methods of Marcelino Bento Soares (Genome Research 6: 791-806, 1996)."

ORIGIN

Query Match 84.0%; Score 16.8; DB 4; Length 569;
 Best Local Similarity 90.0%; Pred. No. 1.6e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20

||||| |||||||

Db 186 ATGGCGTTTCTGAGTAGCAG 167

REFERENCE

CG985592/c

LOCUS

DEFINITION

CG985592

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:39911371

GSS.

Bos taurus

Bos taurus

CG985592.1

GI:3991

DEFINITION BOHZN67TF BO 2.3 KB Brassica oleracea genomic clone BOHZN67, genomic survey sequence.

ACCESSION BH646059
VERSION BH646059.1 GI:18703452
KEYWORDS GSS.

SOURCE Brassica oleracea
ORGANISM Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 645)

Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.

Whole genome shotgun sequencing of Brassica oleracea

Unpublished (2001)

Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TF

Class: sheared ends.

FEATURES
Location/Qualifiers

1..645
/organism="Brassica oleracea"

/mol_type="genomic DNA"

/strain="TO1000DH3"

/db_xref="taxon:3712"

/clone="BOHZN67"

/clone_lib="BO 2.3 KB"

/notes="Vector: pHOsl; Site 1: BstXI; 2-3 kb sheared"

genomic DNA inserted into pHOsl using BstXI linkers"

ORIGIN

Query Match 84.0%; Score 16.8; DB 8; Length 645;
Best Local Similarity 90.0%; Pred. No. 1.7e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGCGCTCTCTGAGTAGCAG 20
||||| |||||||||
DB 354 AGGCTCTCTGAGTAGCAG 335

RESULT 32
AZ966847/c
LOCUS 647 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0237106R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0237106 R, genomic survey sequence.

ACCESSION AZ966847
VERSION AZ966847.1 GI:13838074
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 647)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

FEATURES
source

1..647

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0237106"

/sex="Female"

/lab_host="E. coli strain XL10-Gold, TI-resistant, P-"

/clone_lib="Mouse 10kb plasmid UUGC2M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (female) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

ORIGIN

Query Match 84.0%; Score 16.8; DB 8; Length 647;
Best Local Similarity 90.0%; Pred. No. 1.7e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGCGCTCTCTGAGTAGCAG 20
||||| |||||||||
DB 164 AGGTTTCTCTGAGTAGCAG 145

RESULT 33
AZ840734/c
LOCUS 664 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0138122F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0138122 F, genomic survey sequence.

ACCESSION AZ840734
VERSION AZ840734.1 GI:13010642
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 664)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0138 row: I column: 22
 Seq primer: CCGTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 664.

FEATURES

Location/Qualifiers
 1..664
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0138122"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 84.0%; Score 16.8; DB 8; Length 664;
 Best Local Similarity 90.0%; Pred. No. 1.7e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGGCTCTCAGTAGCAG 20
 ||||| ||||| ||||| |||||
 Db 181 AGGGGACTCGGAGTAGCAG 162

RESULT 34
 CV288705

LOCUS 669 bp mRNA linear EST 23-SEP-2004
 DEFINITION aof01-9ms3-a04 Aof01 Asparagus officinalis cDNA clone
 aof01-9ms3-a04 5', mRNA sequence.

ACCESSION CV288705
 VERSION CV288705.1 GI:52572310

KEYWORDS EST.

SOURCE Asparagus officinalis (garden asparagus)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Asparagales;
 Asparagusaceae; Asparagus.

1 (bases 1 to 669)

REFERENCE dePamphilis, C., Carlson, J., Ma, H., Soltis, D., Soltis, P.,
 Oppenheimer, D., Frohlich, M., Doyle, J., Tanksey, S., Webb, M.,
 Leebens-Mack, J., Landherr, L., Ilut, D. and Wall, K.

Generation of ESTs from early male inflorescences of Asparagus

officinalis

Unpublished (2004)

Contact: Claude dePamphilis or James Leebens-Mack

Mueller Laboratory

Penn State University

208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn

State University, University Park, PA 16802, USA

Tel: 814 863 6413

Fax: 814 865 9131

Email: cwd3@psu.edu or jhl10@psu.edu

The sequence provided is trimmed of vector and low quality regions.

FEATURES

Location/Qualifiers
 1..669
 /organism="Asparagus officinalis"
 /mol_type="mRNA"
 /db_xref="taxon:4686"
 /clone="aof01-9ms3-a04"
 /tissue_type="male inflorescences"
 /lab_host="SOLR"
 /clone_lib="Aof01"

/note="Vector: pBluescript SK (+/-); Site 1: EcoRI;
 Site 2: XhoI; This is a directionally cloned,
 non-normalized library. This library has been generated by
 the Floral Genome Project (FGP). The Floral Genome Project
 is funded by NSF's Plant Genome Research Program
 (DBI-0115684). More information about the project can be
 obtained at http://fgp.bio.psu.edu"

ORIGIN

Query Match 84.0%; Score 16.8; DB 7; Length 669;
 Best Local Similarity 90.0%; Pred. No. 1.7e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGGCTCTCAGTAGCAG 20
 ||||| ||||| ||||| |||||
 Db 380 AGGGGCTCAGATGGCAG 399

RESULT 35
 LOCUS CR191252/c

DEFINITION Reverse strand read from insert in 5'HPRT insertion targeting and
 chromosome engineering clone MHPN109, genomic survey sequence.

ACCESSION CR191252

VERSION CR191252.1 GI:49970101

KEYWORDS GSS; genome survey sequence; MICER.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 679)

REFERENCE Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,
 Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,
 Rogers, J. and Bradley, A.

Direct Submision

Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,

CB10 1SA, UK. http://www.sanger.ac.uk/MICER

FEATURES

Location/Qualifiers
 1..679
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /clone="MHPN109"
 /clone_lib="MHPN"

ORIGIN

Query Match 84.0%; Score 16.8; DB 9; Length 679;
 Best Local Similarity 90.0%; Pred. No. 1.7e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGGCTCTCAGTAGCAG 20
 ||||| ||||| ||||| |||||
 Db 571 AGGGAGTCACTAGTAGCAG 552

RESULT 36
 AV370109

LOCUS AV370109
 DEFINITION AV370109 RIKEN full-length enriched, adult male colon Mus musculus
 cDNA clone 9030207M06 3', mRNA sequence.

Full sequence and original trace file are available from the Plant
 Genome Network website (http://pgn.cornell.edu)
 Plate: aof01-9ms3 row: a Column: 04
 Seq primer: M13F.

```

ACCESSION AV370109
VERSION AV370109.2 GI:16397792
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus

REFERENCE
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Takeda,Y., Tanaka,T., Toyota,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
On Nov 14, 1999 this sequence version replaced gi:6417756.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-resgsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsuura,S., Kawai,Y., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I.,
Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
further details.
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
FEATURES
source
1. .684
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="9030207M06"
/sex="male"
/tissue_type="colon"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, adult male colon"
/notes="Site 1: Sali; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAAGGATCCAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 185.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGATTCTCGAGTTAATTAATTAATCCCCCCCCCC
3']. cDNA was cloned into the XhoI and BamHI sites.
Vector: a modified phluescript KS(+) after bulk excision
from Lambda FLC I. Cloning sites, 5' end: Sali; 3' end:
BamHI"

ORIGIN
Query Match 84.0%; Score 16.8; DB 1; Length 684;
Best Local Similarity 90.0%; Pred. No. 1.7e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
Db 331 AGGGTTCTCTGAGTAGCAG 350

RESULT 37
AG119191
LOCUS AG119191 702 bp DNA linear GSS 03-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-127124.F, genomic survey sequence.
ACCESSION AG119191
VERSION AG119191.1 GI:16739710
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE 1
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
2 (bases 1 to 702)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-cho,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimbescgsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
1. .702
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-127124.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN
Query Match 84.0%; Score 16.8; DB 9; Length 702;
Best Local Similarity 90.0%; Pred. No. 1.7e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20

```


The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the rat BAC library CHORI-230
 (<http://www.chori.org/bacpac/rat230.htm>). For BAC library
 availability, please contact Pieter de Jong (pdejong@mail.cho.org).
 Clones may be purchased from BACPAC Resources
 (http://www.chori.org/bacpac/orering_information.htm). BAC end
 page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
 Plate: 40 row: G column: 3
 Seq primer: SP6
 Class: BAC ends.

FEATURES

source Location/Qualifiers
 1..730
 /organism="Rattus norvegicus"
 /mol_type="genomic DNA"
 /strain="BN/SsNHsd/MCW"
 /db_xref="taxon:10116"
 /clone="CH230-40G3"
 /sex="female"
 /cell_type="Brain"
 /clone_lib="CHORI-230 Segment 1"
 /notes="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
 CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
 Pieter de Jong"

ORIGIN

Query Match 84.0%; Score 16.8; DB 8; Length 730;
 Best Local Similarity 90.0%; Pred. No. 1.7e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
 |||||
 Db 114 AGGGAGTGTCTGAGTAGCAG 133

RESULT 41
 AG383658/c
 LOCUS AG383658 736 bp DNA linear GSS 03-JUN-2004
 DEFINITION Mus musculus molossinus DNA, clone:MSMg01-194019.T7, genomic survey
 sequence.
 ACCESSION AG383658
 VERSION AG383658.1 GI:47994863
 KEYWORDS GSS.
 SOURCE Mus musculus molossinus
 ORGANISM Mus musculus molossinus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
 BAC end Sequences of Library MSMg01

REFERENCE
 AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
 TITLE BAC end Sequences of Library MSMg01
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 736)

Direct Submission
 Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
 Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail:hattori@gsc.riken.jp, URL:<http://hgp.gsc.riken.go.jp/>,
 Tel:81-45-503-9111, Fax:81-45-503-9170)
 Clones are derived from the mouse BAC library MSMg01. For BAC
 library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
 Tsukuba Institute, Bio Resource Center,
 The Institute of Physical and Chemical Research (RIKEN) 3-1-1
 Koyadai, Tsukuba, 305-0074 Japan
 phone: 81-298-36-9189, fax: 81-298-36-9199
 e-mail: abe@rtc.riken.jp
 PRIMERS
 Sequencing : T7
 LIBRARY Vector : pBACe3.6

COMMENT

R.Site 1 : EcoRI
 R.Site 2 : EcoRI.
 Location/Qualifiers
 1..736
 /organism="Mus musculus molossinus"
 /mol_type="genomic DNA"
 /sub_species="molossinus"
 /db_xref="taxon:57486"
 /clone="MSMg01-194019.T7"
 /sex="male"
 /tissue_type="mixture of kidney and spleen"
 /clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN

Query Match 84.0%; Score 16.8; DB 9; Length 736;
 Best Local Similarity 90.0%; Pred. No. 1.7e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
 |||||
 Db 82 AGGGTGTCTCTGAGTAGCTG 63

RESULT 42

AG569158/c
 LOCUS AG569158 744 bp DNA linear GSS 05-JUN-2004
 DEFINITION Mus musculus molossinus DNA, clone:MSMg01-491B06.TJ, genomic survey
 sequence.
 ACCESSION AG569158
 VERSION AG569158.1 GI:48329856
 KEYWORDS GSS.
 SOURCE Mus musculus molossinus
 ORGANISM Mus musculus molossinus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
 BAC end Sequences of Library MSMg01

REFERENCE
 AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
 TITLE BAC end Sequences of Library MSMg01
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 744)

Direct Submission
 Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
 Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail:hattori@gsc.riken.jp, URL:<http://hgp.gsc.riken.go.jp/>,
 Tel:81-45-503-9111, Fax:81-45-503-9170)
 Clones are derived from the mouse BAC library MSMg01. For BAC
 library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
 Tsukuba Institute, Bio Resource Center,
 The Institute of Physical and Chemical Research (RIKEN) 3-1-1
 Koyadai, Tsukuba, 305-0074 Japan
 phone: 81-298-36-9189, fax: 81-298-36-9199
 e-mail: abe@rtc.riken.jp
 PRIMERS
 Sequencing : TJ
 LIBRARY Vector : pBACe3.6
 R.Site 1 : EcoRI.
 R.Site 2 : EcoRI.

FEATURES

source Location/Qualifiers
 1..744
 /organism="Mus musculus molossinus"
 /mol_type="genomic DNA"
 /sub_species="molossinus"
 /db_xref="taxon:57486"
 /clone="MSMg01-491B06.TJ"
 /sex="male"
 /tissue_type="mixture of kidney and spleen"
 /clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN

Query Match 84.0%; Score 16.8; DB 9; Length 744;

```

Best Local Similarity 90.0%; Pred. No. 1.7e+03; Mismatches 2; Indels 0; Gaps 0;
Matches 18; Conservative 0;

QY 1 AGGGGCTCTCTGAGTAGCAG 20
||||| ||||| ||||| |||||
Db 290 AGGGCTCTCTGAGTAACAG 271

RESULT 43
CC552929
LOCUS CH240_438B16.TARBAC13P2 CHORI-240 Bos taurus genomic clone GSS 17-JUN-2003
DEFINITION CH240_438B16, genomic survey sequence.
ACCESSION CC552929
VERSION CC552929.1 GI:31871213
KEYWORDS GSS.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 744)
Holt, R., Scott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L.,
Tsai, M., Cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M., Chiu, R.,
Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R.,
Mathewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S.,
Schein, J., Marra, M., de Jong, P., Keele, J.W. and Kappes, S.M.
Bovine BAC End Sequences from Library CHORI-240, PLATES 399 to 478
Unpublished (2003)
Other_GSSs: CH240_438B16.T7
Contact: Rob Holt
Sequencing
The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
Tel: 604-877-6085
Fax: 604-877-8276
Email: rholt@bccgc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering.information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
Plate: 438 row: B column: 16
Seq primer: SP6
Class: BAC ends.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9913"
                     /clone="CH240_438B16"
                     /sex="Male"
                     /cell_type="Blood"
                     /clone_lib="CHORI-240"
                     /note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
                     Hereford bull I1 Domino 99375; CHORI-240 Bovine BAC
                     library (Male) produced by Pieter de Jong"

ORIGIN
Query Match      84.0%; Score 16.8; DB 9; Length 744;
Best Local Similarity 90.0%; Pred. No. 1.7e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGGCTCTCTGAGTAGCAG 20
||||| ||||| ||||| |||||
Db 460 AGGGTTCTCTGAGTAGCAG 441

RESULT 45
AG591654
LOCUS Mus musculus molossinus DNA, clone:MSMg01-520K21.T7, genomic survey
DEFINITION sequence.
ACCESSION AG591654
VERSION AG591654.1 GI:48352484
KEYWORDS GSS.
SOURCE Mus musculus molossinus
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
BAC end Sequences of Library MSMg01
Unpublished
2 (bases 1 to 773)
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: hattori@psc.riken.jp, URL: http://hgp.psc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.

```


TITLE
JOURNAL
COMMENT

Leebens-Mack, J., Landherr, L., Ilut, D. and Wall, K.
 Generation of ESTs from early male inflorescences of Asparagus officinalis
 Unpublished (2004)
 Contact: Claude dePamphilis or James Leebens-Mack
 Mueller Laboratory
 Penn State University
 208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn State University, University Park, PA 16802, USA
 Tel: 814 863 6413
 Fax: 814 865 9131
 Email: cwd3@psu.edu or jhl10@psu.edu
 The sequence provided is trimmed of vector and low quality regions. Full sequence and original trace file are available from the Plant Genome Network website (<http://pgn.cornell.edu>)
 Plate: aof01-2ms4 row: e column: 12
 Seq primer: M13F.

FEATURES

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 /tissue_type="male inflorescences"
 /lab_host="SOLR"
 /clone_lib="Aof01"
 /notes="Vector: pBluescript SK (+/-); Site 1: EcoRI; Site 2: XhoI; This is a directionally cloned, non-normalized library. This library has been generated by the Floral Genome Project (FGP). The Floral Genome Project is funded by NSF's Plant Genome Research Program (DBI-0115684). More information about the project can be obtained at <http://fgp.bio.psu.edu>"

ORIGIN

Query Match 84.0%; Score 16.8; DB 7; Length 846;
 Best Local Similarity 90.0%; Pred. No. 1.7e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 DB 267 AGGGCGTCTCAGAGTGGCAG 248

RESULT 49
CR802378/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CR802378 855 bp DNA linear GSS 24-SEP-2004
 GR0AAA21DB07FM1 INRA BAC Bos taurus genomic clone INRA_425C11, DNA sequence, genomic survey sequence.
 CR802378
 GSS.
 Bos taurus (cow)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
 1 (bases 1 to 855)
 Eggen, A., Schibler, L. and Roy, A.
 Bovine BAC End Sequences from the INRA bovine BAC library
 Unpublished
 2 (bases 1 to 855)
 Genoscope.
 Direct Submission
 Submitted (20-SEP-2004) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
 - Web : www.genoscope.cns.fr
 Contact: Andre Eggen
 Department of Animal Genetics - LGBC
 INRA
 78350 Jouy-en-Josas, France
 Tel: 33 1 34 65 24 24
 Fax: 33 1 34 65 24 78

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 855)
 Eggen, A., Schibler, L. and Roy, A.
 Bovine BAC End Sequences from the INRA bovine BAC library
 Unpublished
 2 (bases 1 to 855)
 Genoscope.
 Direct Submission
 Submitted (20-SEP-2004) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
 - Web : www.genoscope.cns.fr
 Contact: Andre Eggen
 Department of Animal Genetics - LGBC
 INRA
 78350 Jouy-en-Josas, France
 Tel: 33 1 34 65 24 24
 Fax: 33 1 34 65 24 78

Email: eggen@jouy.inra.fr
 Clones are derived from the INRA bovine BAC library (http://locus.jouy.inra.fr/fpc/cattle_bac_map.htm). For BAC library availability, please contact Andre Eggen (eggen@jouy.inra.fr). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by INRA (Jouy-en-Josas) and Genoscope (Evry) Plate: 425 row: C column: 11
 Seq primer: M13 Forward
 Class: BAC ends.

FEATURES

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 /mol_type="genomic DNA"
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 /note="Vector: pBelOAC11; Site 1: HindIII; Holstein bull; INRA Bovine BAC library (Male) produced by Andre Eggen-Genoscope sequence ID : GR0AAA21DB07FM1"

ORIGIN

Query Match 84.0%; Score 16.8; DB 9; Length 855;
 Best Local Similarity 90.0%; Pred. No. 1.7e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
 |||||
 DB 727 AGGGCGTCTCTGAGTGGCAG 708

RESULT 50

CR194037/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CR194037 874 bp DNA linear GSS 06-JUL-2004
 Reverse strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN354n23, genomic survey sequence.
 CR194037
 CR194037.1 GI:49972886
 GSS; genome survey sequence; MICER.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 874)
 Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J. and Bradley, A.
 Direct Submission
 Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. <http://www.sanger.ac.uk/MICER>

FEATURES
 source
 1. .874
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 /mol_type="genomic DNA"
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ORIGIN

Query Match 84.0%; Score 16.8; DB 9; Length 874;
 Best Local Similarity 90.0%; Pred. No. 1.7e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
 |||||
 DB 571 AGGGAGTCACTGAGTAGCAG 552

Search completed: March 14, 2005, 21:20:08
 Job time : 1968 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 14, 2005, 17:14:07 ; Search time 102 Seconds
(without alignments)
320.839 Million cell updates/sec

Title: US-10-672-399-10

Perfect score: 20

Sequence: 1 agggcgtctctgtagtagcag 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Issued Patents_NA.*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*

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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	100.0	2087	4	US-09-949-016-5659
C 2	20	100.0	2116	3	US-08-635-552A-1
C 3	20	100.0	2117	3	US-09-155-768-1
C 4	20	100.0	14862	4	US-09-949-016-17401
5	16.8	84.0	278	4	US-09-513-999C-14085
6	16.8	84.0	313	4	US-09-513-999C-2290
7	15.8	79.0	525	4	US-09-904-196B-2
8	15.8	79.0	525	4	US-09-760-008A-2
9	15.8	79.0	525	4	US-10-192-294-2
10	15.8	79.0	601	4	US-09-949-016-62651
11	15.8	79.0	601	4	US-09-949-016-62652
12	15.8	79.0	601	4	US-09-949-016-62687
13	15.8	79.0	601	4	US-09-949-016-62688
14	15.8	79.0	601	4	US-09-949-016-88843
15	15.8	79.0	601	4	US-09-949-016-88844
16	15.8	79.0	882	4	US-09-253-991A-10864
C 17	15.8	79.0	972	4	US-09-902-540-5986
18	15.8	79.0	1203	4	US-09-252-991A-10820
19	15.8	79.0	1315	4	US-09-902-540-215
C 20	15.8	79.0	2614	2	US-08-795-868-15
C 21	15.8	79.0	2614	3	US-09-303-069-15
C 22	15.8	79.0	2614	3	US-09-134-250-15
C 23	15.8	79.0	5000	4	US-09-791-105B-1
C 24	15.8	79.0	37792	4	US-09-949-016-12503
C 25	15.8	79.0	37795	4	US-09-949-016-14263
26	15.8	79.0	46085	4	US-09-949-016-13547
27	15.8	79.0	46085	4	US-09-949-016-13548

28	15.8	79.0	114793	4	US-10-148-806-3	Sequence 3, Appli
C 29	15.8	79.0	118999	3	US-09-791-105B-32	Sequence 32, Appl
30	15.8	79.0	403765	3	US-09-103-840A-2	Sequence 2, Appli
31	15.8	79.0	4411529	3	US-09-103-840A-1	Sequence 1, Appli
32	15.4	77.0	40546	4	US-09-949-016-12847	Sequence 12847, A
33	15.4	77.0	40546	4	US-09-949-016-12915	Sequence 12915, A
34	15.4	77.0	70014	4	US-09-949-016-17110	Sequence 17110, A
C 35	15.4	77.0	155019	4	US-09-949-016-16029	Sequence 16029, A
C 36	15.2	76.0	25	4	US-09-396-196G-69161	Sequence 69161, A
C 37	15.2	76.0	499	4	US-09-513-999C-809	Sequence 809, App
38	15.2	76.0	499	4	US-09-270-767-1373	Sequence 1973, Ap
39	15.2	76.0	526	4	US-09-270-767-17255	Sequence 17255, A
C 40	15.2	76.0	597	4	US-09-270-767-5447	Sequence 5447, Ap
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C 45	15.2	76.0	601	4	US-09-949-016-167671	Sequence 167671, A
46	15.2	76.0	606	4	US-09-252-991A-607	Sequence 607, App
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C 48	15.2	76.0	1164	4	US-09-902-540-8443	Sequence 8443, Ap
C 49	15.2	76.0	1182	4	US-09-252-991A-520	Sequence 520, App
50	15.2	76.0	1219	4	US-09-270-767-28815	Sequence 28815, A
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C 52	15.2	76.0	1299	4	US-09-252-991A-496	Sequence 496, App
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C 54	15.2	76.0	1434	4	US-10-177-661-1	Sequence 1, Appli
C 55	15.2	76.0	1551	4	US-09-902-540-6712	Sequence 6712, Ap
56	15.2	76.0	1731	4	US-09-270-767-13778	Sequence 13778, A
C 57	15.2	76.0	1748	4	US-09-879-792-11	Sequence 11, Appl
58	15.2	76.0	2640	4	US-09-270-767-504	Sequence 504, App
59	15.2	76.0	2640	4	US-09-270-767-15786	Sequence 15786, A
C 60	15.2	76.0	2643	3	US-09-399-913-56	Sequence 56, Appl
C 61	15.2	76.0	2643	3	US-09-350-614-56	Sequence 56, Appl
62	15.2	76.0	4019	4	US-09-902-540-535	Sequence 535, App
C 63	15.2	76.0	7515	4	US-09-902-540-888	Sequence 888, App
C 64	15.2	76.0	16365	4	US-09-949-016-16970	Sequence 16970, A
65	15.2	76.0	20378	4	US-09-949-016-17281	Sequence 17281, A
66	15.2	76.0	36171	4	US-09-949-016-13876	Sequence 13876, A
67	15.2	76.0	36274	4	US-09-949-016-12389	Sequence 12389, A
C 68	15.2	76.0	74730	4	US-09-949-016-15189	Sequence 15189, A
69	15.2	76.0	78157	4	US-09-949-016-16466	Sequence 16466, A
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C 71	15.2	76.0	149543	4	US-09-949-016-15947	Sequence 15947, A
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77	14.8	74.0	601	4	US-09-949-016-182417	Sequence 182417, A
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C 80	14.8	74.0	1089	4	US-09-252-991A-9990	Sequence 9990, Ap
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82	14.8	74.0	1254	3	US-08-952-014C-49	Sequence 49, Appl
83	14.8	74.0	3396	4	US-09-614-221A-530	Sequence 530, App
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86	14.8	74.0	5912	3	US-08-952-127-1	Sequence 1, Appli
87	14.8	74.0	5912	3	US-08-952-014C-1	Sequence 1, Appli
88	14.8	74.0	6525	1	US-08-493-092-3	Sequence 3, Appli
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90	14.8	74.0	7408	1	US-08-441-832-1	Sequence 1, Appli
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92	14.8	74.0	7410	1	US-08-508-836A-1	Sequence 1, Appli
93	14.8	74.0	9171	2	US-08-629-001A-2	Sequence 2, Appli
94	14.8	74.0	9171	3	US-08-642-274D-2	Sequence 2, Appli
95	14.8	74.0	9171	3	US-08-952-127-2	Sequence 2, Appli
96	14.8	74.0	9171	3	US-08-952-014C-2	Sequence 2, Appli
97	14.8	74.0	9196	4	US-08-984-090-1	Sequence 1, Appli
98	14.8	74.0	9385	2	US-08-874-266-1	Sequence 1, Appli
99	14.8	74.0	9385	3	US-09-360-416-1	Sequence 1, Appli
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C 102	14.8	74.0	16198	4	US-09-949-016-11854	Sequence 11854, A	C 175	14.2	71.0	601	4	US-09-949-016-100145	Sequence 100145, A
C 103	14.8	74.0	16198	4	US-09-949-016-15579	Sequence 15579, A	C 176	14.2	71.0	601	4	US-09-949-016-100146	Sequence 100146, A
C 104	14.8	74.0	16198	4	US-09-949-016-16973	Sequence 16973, A	C 177	14.2	71.0	601	4	US-09-949-016-100411	Sequence 100411, A
C 105	14.8	74.0	28198	4	US-09-949-016-12349	Sequence 12349, A	C 178	14.2	71.0	601	4	US-09-949-016-100412	Sequence 100412, A
C 106	14.8	74.0	30310	4	US-09-657-346A-96	Sequence 96, Appl1	C 179	14.2	71.0	601	4	US-09-949-016-100677	Sequence 100677, A
C 107	14.8	74.0	56131	4	US-09-949-016-12944	Sequence 12944, A	C 180	14.2	71.0	601	4	US-09-949-016-100678	Sequence 100678, A
C 108	14.8	74.0	136058	4	US-09-949-016-12565	Sequence 12565, A	C 181	14.2	71.0	601	4	US-09-949-016-100981	Sequence 100981, A
C 109	14.8	74.0	136480	4	US-09-949-016-17064	Sequence 17064, A	C 182	14.2	71.0	601	4	US-09-949-016-100982	Sequence 100982, A
C 110	14.8	74.0	146401	4	US-09-949-016-16151	Sequence 16151, A	C 183	14.2	71.0	601	4	US-09-949-016-101247	Sequence 101247, A
C 111	14.8	74.0	153642	4	US-09-949-016-12174	Sequence 12174, A	C 184	14.2	71.0	601	4	US-09-949-016-101248	Sequence 101248, A
C 112	14.8	74.0	153643	4	US-09-949-016-15635	Sequence 15635, A	C 185	14.2	71.0	601	4	US-09-949-016-101513	Sequence 101513, A
C 113	14.8	74.0	202111	4	US-09-949-016-13877	Sequence 13877, A	C 186	14.2	71.0	601	4	US-09-949-016-101514	Sequence 101514, A
C 114	14.8	74.0	254366	4	US-09-822-871-3	Sequence 3, Appl1	C 187	14.2	71.0	601	4	US-09-949-016-101779	Sequence 101779, A
C 115	14.4	72.0	365	4	US-09-621-976-12759	Sequence 12759, A	C 188	14.2	71.0	601	4	US-09-949-016-101780	Sequence 101780, A
C 116	14.4	72.0	601	4	US-09-949-016-47639	Sequence 47639, A	C 189	14.2	71.0	601	4	US-09-949-016-109883	Sequence 109883, A
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C 118	14.4	72.0	987	4	US-10-061-943A-4	Sequence 4, Appl1	C 191	14.2	71.0	601	4	US-09-949-016-115256	Sequence 115256, A
C 119	14.4	72.0	1441	4	US-09-220-132-39	Sequence 39, Appl1	C 192	14.2	71.0	601	4	US-09-949-016-117714	Sequence 117714, A
C 120	14.4	72.0	4441	4	US-09-949-016-15325	Sequence 15325, A	C 193	14.2	71.0	601	4	US-09-949-016-117731	Sequence 117731, A
C 121	14.4	72.0	5654	4	US-09-573-080A-41	Sequence 41, Appl1	C 194	14.2	71.0	601	4	US-09-949-016-117732	Sequence 117732, A
C 122	14.4	72.0	58782	4	US-09-949-016-16851	Sequence 16851, A	C 195	14.2	71.0	601	4	US-09-949-016-117733	Sequence 117733, A
C 123	14.4	72.0	76472	4	US-09-949-016-15896	Sequence 15896, A	C 196	14.2	71.0	601	4	US-09-949-016-139851	Sequence 139851, A
C 124	14.4	72.0	92276	4	US-09-949-016-12166	Sequence 12166, A	C 197	14.2	71.0	601	4	US-09-949-016-139868	Sequence 139868, A
C 125	14.4	72.0	112339	4	US-09-949-016-13144	Sequence 13144, A	C 198	14.2	71.0	601	4	US-09-949-016-139869	Sequence 139869, A
C 126	14.4	72.0	1830121	4	US-09-557-884-1	Sequence 1, Appl1	C 199	14.2	71.0	601	4	US-09-949-016-139870	Sequence 139870, A
C 127	14.4	72.0	1830121	4	US-09-643-990A-1	Sequence 17, Appl1	C 200	14.2	71.0	601	4	US-09-949-016-168930	Sequence 168930, A
C 128	14.2	71.0	30	3	US-09-052-469-17	Sequence 17, Appl1	C 201	14.2	71.0	601	4	US-09-949-016-168932	Sequence 168932, A
C 129	14.2	71.0	30	4	US-08-422-582-17	Sequence 17, Appl1	C 202	14.2	71.0	711	4	US-09-252-991A-12195	Sequence 12195, A
C 130	14.2	71.0	30	4	US-09-052-262-17	Sequence 17, Appl1	C 203	14.2	71.0	714	4	US-09-252-991A-10604	Sequence 10604, A
C 131	14.2	71.0	315	3	US-08-945-424-1	Sequence 1, Appl1	C 204	14.2	71.0	816	4	US-09-252-991A-10249	Sequence 10249, A
C 132	14.2	71.0	330	1	US-08-718-865-1	Sequence 1, Appl1	C 205	14.2	71.0	870	4	US-09-902-540-6646	Sequence 6646, Ap
C 133	14.2	71.0	330	1	US-08-620-467A-7	Sequence 7, Appl1	C 206	14.2	71.0	991	4	US-09-439-554-27	Sequence 27, Appl1
C 134	14.2	71.0	330	3	US-09-041-090B-7	Sequence 7, Appl1	C 207	14.2	71.0	1000	1	US-07-960-112B-1	Sequence 1, Appl1
C 135	14.2	71.0	330	3	US-08-442-001C-7	Sequence 7, Appl1	C 208	14.2	71.0	1000	1	US-07-960-112B-3	Sequence 3, Appl1
C 136	14.2	71.0	330	4	US-08-513-999C-35305	Sequence 35305, A	C 209	14.2	71.0	1000	1	US-08-301-316B-1	Sequence 1, Appl1
C 137	14.2	71.0	356	4	US-08-943-731-198	Sequence 198, App	C 210	14.2	71.0	1000	1	US-08-301-316B-3	Sequence 3, Appl1
C 138	14.2	71.0	420	3	US-09-949-016-21345	Sequence 21345, A	C 211	14.2	71.0	1000	2	US-08-473-399B-1	Sequence 1, Appl1
C 139	14.2	71.0	601	4	US-09-949-016-21345	Sequence 21345, A	C 212	14.2	71.0	1000	2	US-08-473-399B-3	Sequence 3, Appl1
C 140	14.2	71.0	601	4	US-09-949-016-57870	Sequence 57870, A	C 213	14.2	71.0	1000	3	US-08-853-831-1	Sequence 1, Appl1
C 141	14.2	71.0	601	4	US-09-949-016-57871	Sequence 57871, A	C 214	14.2	71.0	1000	3	US-08-853-831-3	Sequence 3, Appl1
C 142	14.2	71.0	601	4	US-09-949-016-69385	Sequence 69385, A	C 215	14.2	71.0	1000	3	US-09-510-885-1	Sequence 1, Appl1
C 143	14.2	71.0	601	4	US-09-949-016-69386	Sequence 69386, A	C 216	14.2	71.0	1000	4	US-09-510-885-3	Sequence 3, Appl1
C 144	14.2	71.0	601	4	US-09-949-016-74337	Sequence 74337, A	C 217	14.2	71.0	1000	5	PCT-US93-09774-1	Sequence 1, Appl1
C 145	14.2	71.0	601	4	US-09-949-016-80719	Sequence 80719, A	C 218	14.2	71.0	1000	5	PCT-US93-09774-3	Sequence 3, Appl1
C 146	14.2	71.0	601	4	US-09-949-016-80720	Sequence 80720, A	C 219	14.2	71.0	1149	4	US-09-252-991A-12262	Sequence 12262, A
C 147	14.2	71.0	601	4	US-09-949-016-96421	Sequence 96421, A	C 220	14.2	71.0	1150	4	US-09-931-401B-1	Sequence 1, Appl1
C 148	14.2	71.0	601	4	US-09-949-016-96422	Sequence 96422, A	C 221	14.2	71.0	1251	4	US-09-252-991A-12303	Sequence 12303, A
C 149	14.2	71.0	601	4	US-09-949-016-96687	Sequence 96687, A	C 222	14.2	71.0	1278	4	US-09-252-991A-12121	Sequence 12121, A
C 150	14.2	71.0	601	4	US-09-949-016-96688	Sequence 96688, A	C 223	14.2	71.0	1356	1	US-08-143-497-1	Sequence 1, Appl1
C 151	14.2	71.0	601	4	US-09-949-016-96953	Sequence 96953, A	C 224	14.2	71.0	1356	1	US-08-461-666-1	Sequence 1, Appl1
C 152	14.2	71.0	601	4	US-09-949-016-96954	Sequence 96954, A	C 225	14.2	71.0	1356	1	US-08-463-675-1	Sequence 1, Appl1
C 153	14.2	71.0	601	4	US-09-949-016-97219	Sequence 97219, A	C 226	14.2	71.0	1356	1	US-08-757-300-1	Sequence 1, Appl1
C 154	14.2	71.0	601	4	US-09-949-016-97220	Sequence 97220, A	C 227	14.2	71.0	1356	1	US-08-757-300-1	Sequence 1, Appl1
C 155	14.2	71.0	601	4	US-09-949-016-97485	Sequence 97485, A	C 228	14.2	71.0	1356	1	US-08-464-589-1	Sequence 1, Appl1
C 156	14.2	71.0	601	4	US-09-949-016-97486	Sequence 97486, A	C 229	14.2	71.0	1386	4	US-09-252-991A-10462	Sequence 10462, A
C 157	14.2	71.0	601	4	US-09-949-016-97751	Sequence 97751, A	C 230	14.2	71.0	1497	4	US-09-799-451-127	Sequence 127, App
C 158	14.2	71.0	601	4	US-09-949-016-97752	Sequence 97752, A	C 231	14.2	71.0	1668	3	US-09-976-594-336	Sequence 336, Appl
C 159	14.2	71.0	601	4	US-09-949-016-98017	Sequence 98017, A	C 232	14.2	71.0	1756	3	US-09-166-350-30	Sequence 30, Appl
C 160	14.2	71.0	601	4	US-09-949-016-98018	Sequence 98018, A	C 233	14.2	71.0	1756	4	US-09-023-655-954	Sequence 954, App
C 161	14.2	71.0	601	4	US-09-949-016-98283	Sequence 98283, A	C 234	14.2	71.0	2613	4	US-09-949-016-5563	Sequence 5563, App
C 162	14.2	71.0	601	4	US-09-949-016-98284	Sequence 98284, A	C 235	14.2	71.0	2727	4	US-09-949-016-1154	Sequence 1154, Ap
C 163	14.2	71.0	601	4	US-09-949-016-98549	Sequence 98549, A	C 236	14.2	71.0	2878	1	US-07-903-456-1	Sequence 1, Appl1
C 164	14.2	71.0	601	4	US-09-949-016-98550	Sequence 98550, A	C 237	14.2	71.0	2878	3	US-08-666-221B-5	Sequence 5, Appl1
C 165	14.2	71.0	601	4	US-09-949-016-98815	Sequence 98815, A	C 238	14.2	71.0	2878	3	US-08-666-221B-11	Sequence 11, Appl
C 166	14.2	71.0	601	4	US-09-949-016-98816	Sequence 98816, A	C 239	14.2	71.0	2878	3	US-08-666-221B-13	Sequence 13, Appl
C 167	14.2	71.0	601	4	US-09-949-016-99081	Sequence 99081, A	C 240	14.2	71.0	3018	3	US-08-249-241-1	Sequence 1, Appl1
C 168	14.2	71.0	601	4	US-09-949-016-99082	Sequence 99082, A	C 241	14.2	71.0	3131	4	US-09-051-961-1	Sequence 1, Appl1
C 169	14.2	71.0	601	4	US-09-949-016-99347	Sequence 99347, A	C 242	14.2	71.0	3540	3	US-09-902-540-513	Sequence 513, App
C 170	14.2	71.0	601	4	US-09-949-016-99348	Sequence 99348, A	C 243	14.2	71.0	3540	3	US-08-842-079-16	Sequence 16, Appl
C 171	14.2	71.0	601	4	US-09-949-016-99613	Sequence 99613, A	C 244	14.2	71.0	4220	3	US-09-638-857-16	Sequence 16, Appl
C 172	14.2	71.0	601	4	US-09-949-016-99614	Sequence 99614, A	C 245	14.2	71.0	4220	3	US-09-183-846A-11	Sequence 11, Appl
C 173	14.2	71.0	601	4	US-09-949-016-99879	Sequence 99879, A	C 246	14.2	71.0	4220	3	US-08-961-578C-11	Sequence 11, Appl

247	14.2	71.0	4220	4	US-09-670-216-11	Sequence 11, Appl	320	14.2	71.0	818128	4	US-09-949-016-14560	Sequence 14560, A
248	14.2	71.0	4262	4	US-09-949-016-2134	Sequence 2134, Ap	321	14.2	71.0	818128	4	US-09-949-016-14561	Sequence 14561, A
249	14.2	71.0	4322	4	US-09-949-016-647	Sequence 647, App	322	14.2	71.0	818128	4	US-09-949-016-14562	Sequence 14562, A
250	14.2	71.0	4608	1	US-07-718-575-11	Sequence 11, Appl	323	14.2	71.0	818128	4	US-09-949-016-14564	Sequence 14564, A
251	14.2	71.0	4608	1	US-08-481-206-11	Sequence 11, Appl	324	14.2	71.0	818128	4	US-09-949-016-14565	Sequence 14565, A
252	14.2	71.0	4608	2	US-08-486-289A-11	Sequence 11, Appl	325	14.2	71.0	818128	4	US-09-949-016-14566	Sequence 14566, A
253	14.2	71.0	7090	4	US-09-714-550-18	Sequence 18, Appl	326	14.2	71.0	818128	4	US-09-949-016-14567	Sequence 14567, A
254	14.2	71.0	7881	2	US-08-751-189-1	Sequence 1, Appl	327	14	70.0	601	4	US-09-949-016-14568	Sequence 14568, A
255	14.2	71.0	7881	3	US-09-060-836-1	Sequence 1, Appl	328	14	70.0	601	4	US-09-949-016-14569	Sequence 14569, A
256	14.2	71.0	7881	3	US-09-184-445-1	Sequence 1, Appl	329	14	70.0	78720	4	US-09-949-016-14570	Sequence 14570, A
257	14.2	71.0	9442	4	US-09-949-016-12571	Sequence 12571, A	330	14	70.0	78720	4	US-09-949-016-12710	Sequence 12710, A
258	14.2	71.0	9443	4	US-09-949-016-15877	Sequence 15877, A	331	14	70.0	91062	4	US-09-949-016-17283	Sequence 17283, A
259	14.2	71.0	13941	4	US-09-799-451-341	Sequence 341, App	332	14	70.0	264665	4	US-09-949-016-13019	Sequence 13019, A
260	14.2	71.0	14148	3	US-09-422-469-7	Sequence 7, Appl	333	14	70.0	321022	4	US-09-949-016-11852	Sequence 11852, A
261	14.2	71.0	14148	4	US-08-452-582-7	Sequence 7, Appl	334	14	70.0	321022	4	US-09-949-016-14166	Sequence 14166, A
262	14.2	71.0	14148	4	US-09-052-262-7	Sequence 7, Appl	335	14	70.0	784019	4	US-09-949-016-14033	Sequence 14033, A
263	14.2	71.0	15449	4	US-09-949-016-13600	Sequence 13600, A	336	14	70.0	828152	4	US-09-949-016-12777	Sequence 12777, A
264	14.2	71.0	15356	4	US-09-949-016-13505	Sequence 13505, A	337	13.8	69.0	25	4	US-09-396-156G-73500	Sequence 73500, A
265	14.2	71.0	17082	4	US-09-949-016-14893	Sequence 14893, A	338	13.8	69.0	119	4	US-09-513-999C-19383	Sequence 19383, A
266	14.2	71.0	20084	3	US-08-943-731-5	Sequence 5, Appl	339	13.8	69.0	312	4	US-09-270-767-26747	Sequence 26747, A
267	14.2	71.0	21526	4	US-09-949-016-14685	Sequence 14685, A	340	13.8	69.0	485	5	PCT-US95-05741-10	Sequence 10, Appl
268	14.2	71.0	31571	1	US-08-323-443B-1	Sequence 1, Appl	341	13.8	69.0	551	4	US-09-949-016-84434	Sequence 84434, A
269	14.2	71.0	35871	4	US-09-956-335-2	Sequence 2, Appl	342	13.8	69.0	593	4	US-09-270-767-10755	Sequence 10755, A
270	14.2	71.0	35935	2	US-08-735-609-1	Sequence 1, Appl	343	13.8	69.0	601	4	US-09-949-016-48801	Sequence 48801, A
271	14.2	71.0	35935	2	US-08-735-609-1	Sequence 1, Appl	344	13.8	69.0	601	4	US-09-949-016-48802	Sequence 48802, A
272	14.2	71.0	35935	3	US-08-378-452-43	Sequence 43, Appl	345	13.8	69.0	601	4	US-09-949-016-48803	Sequence 48803, A
273	14.2	71.0	35935	3	US-09-315-372-1	Sequence 1, Appl	346	13.8	69.0	601	4	US-09-949-016-48973	Sequence 48973, A
274	14.2	71.0	35935	3	US-09-248-752-1	Sequence 1, Appl	347	13.8	69.0	601	4	US-09-949-016-48974	Sequence 48974, A
275	14.2	71.0	35935	3	US-09-245-437-1	Sequence 1, Appl	348	13.8	69.0	601	4	US-09-949-016-48975	Sequence 48975, A
276	14.2	71.0	35935	3	US-09-409-670-43	Sequence 43, Appl	349	13.8	69.0	601	4	US-09-949-016-49145	Sequence 49145, A
277	14.2	71.0	35935	3	US-09-562-919-1	Sequence 1, Appl	350	13.8	69.0	601	4	US-09-949-016-49146	Sequence 49146, A
278	14.2	71.0	35978	4	US-09-956-335-1	Sequence 1, Appl	351	13.8	69.0	601	4	US-09-949-016-49147	Sequence 49147, A
279	14.2	71.0	39498	4	US-09-949-016-12410	Sequence 12410, A	352	13.8	69.0	601	4	US-09-949-016-49321	Sequence 49321, A
280	14.2	71.0	39498	4	US-09-949-016-16505	Sequence 16505, A	353	13.8	69.0	601	4	US-09-949-016-49322	Sequence 49322, A
281	14.2	71.0	46253	4	US-09-949-016-11890	Sequence 11890, A	354	13.8	69.0	601	4	US-09-949-016-49323	Sequence 49323, A
282	14.2	71.0	46257	4	US-09-949-016-13711	Sequence 13711, A	355	13.8	69.0	601	4	US-09-949-016-61189	Sequence 61189, A
283	14.2	71.0	49399	4	US-09-949-016-13780	Sequence 13780, A	356	13.8	69.0	601	4	US-09-949-016-84433	Sequence 84433, A
284	14.2	71.0	50186	4	US-09-949-016-14066	Sequence 14066, A	357	13.8	69.0	601	4	US-09-949-016-85018	Sequence 85018, A
285	14.2	71.0	53266	3	US-08-658-136-2	Sequence 2, Appl	358	13.8	69.0	601	4	US-09-949-016-85169	Sequence 85169, A
286	14.2	71.0	53577	3	US-08-658-136-1	Sequence 1, Appl	359	13.8	69.0	601	4	US-09-949-016-108602	Sequence 108602, A
287	14.2	71.0	60276	4	US-09-949-016-15004	Sequence 15004, A	360	13.8	69.0	601	4	US-09-949-016-120797	Sequence 120797, A
288	14.2	71.0	60338	4	US-09-949-016-15694	Sequence 15694, A	361	13.8	69.0	601	4	US-09-949-016-163641	Sequence 163641, A
289	14.2	71.0	84761	4	US-09-949-016-11919	Sequence 11919, A	362	13.8	69.0	601	4	US-09-949-016-163642	Sequence 163642, A
290	14.2	71.0	84763	4	US-09-949-016-13914	Sequence 13914, A	363	13.8	69.0	601	4	US-09-949-016-168931	Sequence 168931, A
291	14.2	71.0	92681	4	US-09-949-016-14772	Sequence 14772, A	364	13.8	69.0	601	4	US-09-949-016-182411	Sequence 182411, A
292	14.2	71.0	109038	4	US-09-949-016-12199	Sequence 12199, A	365	13.8	69.0	601	4	US-09-949-016-159885	Sequence 159885, A
293	14.2	71.0	118955	4	US-09-949-016-17565	Sequence 17565, A	366	13.8	69.0	601	4	US-09-949-016-199886	Sequence 199886, A
294	14.2	71.0	117001	4	US-09-949-016-15684	Sequence 15684, A	367	13.8	69.0	613	3	US-09-149-476-15	Sequence 15, Appl
295	14.2	71.0	126176	4	US-09-949-016-16137	Sequence 16137, A	368	13.8	69.0	992	4	US-09-270-767-11212	Sequence 11212, A
296	14.2	71.0	126176	4	US-09-949-016-16138	Sequence 16138, A	369	13.8	69.0	1352	1	US-08-552-142A-10	Sequence 10, Appl
297	14.2	71.0	137226	4	US-09-949-016-13763	Sequence 13763, A	370	13.8	69.0	1408	2	US-08-222-124-10	Sequence 10, Appl
298	14.2	71.0	140925	4	US-09-949-016-11777	Sequence 11777, A	371	13.8	69.0	1408	2	US-08-842-657A-10	Sequence 10, Appl
299	14.2	71.0	140982	4	US-09-949-016-16295	Sequence 16295, A	372	13.8	69.0	1414	1	US-08-222-124-9	Sequence 9, Appl
300	14.2	71.0	162914	4	US-09-949-016-15578	Sequence 15578, A	373	13.8	69.0	1414	1	US-08-842-657A-9	Sequence 9, Appl
301	14.2	71.0	236474	4	US-09-949-016-13418	Sequence 13418, A	374	13.8	69.0	1535	1	US-08-910-973-10	Sequence 10, Appl
302	14.2	71.0	254405	4	US-09-949-016-14381	Sequence 14381, A	375	13.8	69.0	1535	1	US-09-499-227-10	Sequence 10, Appl
303	14.2	71.0	258775	4	US-09-949-016-16435	Sequence 16435, A	376	13.8	69.0	1550	3	US-09-234-332-3	Sequence 3, Appl
304	14.2	71.0	451924	4	US-09-949-016-12896	Sequence 12896, A	377	13.8	69.0	1656	3	US-08-318-039A-2	Sequence 2, Appl
305	14.2	71.0	451925	4	US-09-949-016-17305	Sequence 17305, A	378	13.8	69.0	1656	3	US-08-318-038D-16	Sequence 16, Appl
306	14.2	71.0	818128	4	US-09-949-016-14546	Sequence 14546, A	379	13.8	69.0	1656	3	US-08-227-496C-20	Sequence 20, Appl
307	14.2	71.0	818128	4	US-09-949-016-14547	Sequence 14547, A	380	13.8	69.0	1656	3	US-08-435-568A-2	Sequence 2, Appl
308	14.2	71.0	818128	4	US-09-949-016-14548	Sequence 14548, A	381	13.8	69.0	2400	4	US-09-248-796A-2698	Sequence 2698, Ap
309	14.2	71.0	818128	4	US-09-949-016-14549	Sequence 14549, A	382	13.8	69.0	2518	4	US-09-799-451-827	Sequence 827, App
310	14.2	71.0	818128	4	US-09-949-016-14550	Sequence 14550, A	383	13.8	69.0	2586	4	US-10-101-464A-883	Sequence 883, App
311	14.2	71.0	818128	4	US-09-949-016-14551	Sequence 14551, A	384	13.8	69.0	2986	3	US-09-062-416-1	Sequence 1, Appl
312	14.2	71.0	818128	4	US-09-949-016-14552	Sequence 14552, A	385	13.8	69.0	3003	4	US-09-023-655-1115	Sequence 1115, Ap
313	14.2	71.0	818128	4	US-09-949-016-14553	Sequence 14553, A	386	13.8	69.0	3016	2	US-08-344-155C-97	Sequence 97, Appl
314	14.2	71.0	818128	4	US-09-949-016-14554	Sequence 14554, A	387	13.8	69.0	3017	3	US-09-009-490A-86	Sequence 86, Appl
315	14.2	71.0	818128	4	US-09-949-016-14555	Sequence 14555, A	388	13.8	69.0	3024	6	5284931-1	Patent No. 5284931
316	14.2	71.0	818128	4	US-09-949-016-14556	Sequence 14556, A	389	13.8	69.0	3024	6	5284931-1	Patent No. 5284931
317	14.2	71.0	818128	4	US-09-949-016-14557	Sequence 14557, A	390	13.8	69.0	3100	4	US-09-741-238-15	Sequence 15, Appl
318	14.2	71.0	818128	4	US-09-949-016-14558	Sequence 14558, A	391	13.8	69.0	3226	3	US-08-539-205A-5	Sequence 5, Appl
319	14.2	71.0	818128	4	US-09-949-016-14559	Sequence 14559, A	392	13.8	69.0	3226	4	US-09-392-163A-5	Sequence 5, Appl

C 393	13.8	69.0	4899	4	US-09-799-451-714	Sequence 714, App	466	13.8	69.0	524032	4	US-09-949-016-16928	Sequence 16928, A
C 394	13.8	69.0	7266	4	US-09-949-016-16428	Sequence 16428, A	C 467	13.8	69.0	524032	4	US-09-949-016-16928	Sequence 16928, A
C 395	13.8	69.0	7386	4	US-09-949-016-13287	Sequence 13287, A	C 468	13.8	69.0	524032	4	US-09-949-016-16929	Sequence 16929, A
C 396	13.8	69.0	8396	3	US-09-328-174A-1	Sequence 1, Appl	C 469	13.8	69.0	524032	4	US-09-949-016-16929	Sequence 16929, A
C 397	13.8	69.0	8409	3	US-09-167-681-37	Sequence 37, Appl	C 470	13.8	69.0	524032	4	US-09-949-016-16930	Sequence 16930, A
C 398	13.8	69.0	13634	4	US-09-949-016-16376	Sequence 16376, A	C 471	13.8	69.0	524032	4	US-09-949-016-16930	Sequence 16930, A
C 399	13.8	69.0	13906	4	US-09-949-016-14730	Sequence 14730, A	C 472	13.8	69.0	524032	4	US-09-949-016-16931	Sequence 16931, A
C 400	13.8	69.0	14340	4	US-09-949-016-16972	Sequence 16972, A	C 473	13.8	69.0	524032	4	US-09-949-016-16931	Sequence 16931, A
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C 402	13.8	69.0	18302	4	US-09-949-016-13163	Sequence 13163, A	C 475	13.8	69.0	529885	4	US-09-949-016-14340	Sequence 14340, A
C 403	13.8	69.0	22120	4	US-09-949-016-16637	Sequence 16637, A	C 476	13.8	69.0	529885	4	US-09-949-016-14341	Sequence 14341, A
C 404	13.8	69.0	23578	4	US-09-949-016-14160	Sequence 14160, A	C 477	13.8	69.0	529885	4	US-09-949-016-14341	Sequence 14341, A
C 405	13.8	69.0	28555	4	US-09-949-016-13106	Sequence 13106, A	C 478	13.8	69.0	529885	4	US-09-949-016-14342	Sequence 14342, A
C 406	13.8	69.0	31469	4	US-09-949-016-13722	Sequence 13722, A	C 479	13.8	69.0	529885	4	US-09-949-016-14342	Sequence 14342, A
C 407	13.8	69.0	36307	4	US-09-949-016-17372	Sequence 17372, A	C 480	13.8	69.0	529885	4	US-09-949-016-14343	Sequence 14343, A
C 408	13.8	69.0	40037	4	US-09-949-016-17375	Sequence 12715, A	C 481	13.8	69.0	529885	4	US-09-949-016-14343	Sequence 14343, A
C 409	13.8	69.0	42003	4	US-10-081-563-25	Sequence 25, Appl	C 482	13.8	69.0	529885	4	US-09-949-016-14344	Sequence 14344, A
C 410	13.8	69.0	43435	4	US-09-949-016-13909	Sequence 12909, A	C 483	13.8	69.0	529885	4	US-09-949-016-14344	Sequence 14344, A
C 411	13.8	69.0	44821	4	US-09-949-016-13764	Sequence 13764, A	C 484	13.8	69.0	529885	4	US-09-949-016-14345	Sequence 14345, A
C 412	13.8	69.0	54420	4	US-09-949-016-15422	Sequence 15422, A	C 485	13.8	69.0	529885	4	US-09-949-016-14345	Sequence 14345, A
C 413	13.8	69.0	54779	4	US-09-949-001-27	Sequence 27, Appl	C 486	13.8	69.0	529885	4	US-09-949-016-14346	Sequence 14346, A
C 414	13.8	69.0	54780	4	US-09-949-001-39	Sequence 39, Appl	C 487	13.8	69.0	529885	4	US-09-949-016-14346	Sequence 14346, A
C 415	13.8	69.0	57280	4	US-09-949-016-11796	Sequence 11796, A	C 488	13.8	69.0	529885	4	US-09-949-016-14347	Sequence 14347, A
C 416	13.8	69.0	57280	4	US-09-949-016-12843	Sequence 12843, A	C 489	13.8	69.0	529885	4	US-09-949-016-14347	Sequence 14347, A
C 417	13.8	69.0	57280	4	US-09-949-016-12844	Sequence 12844, A	C 490	13.6	68.0	51	4	US-09-443-199C-287	Sequence 287, App
C 418	13.8	69.0	57280	4	US-09-949-016-12846	Sequence 12846, A	C 491	13.6	68.0	67	4	US-09-474-699-7	Sequence 7, Appl
C 419	13.8	69.0	57280	4	US-09-949-016-13542	Sequence 13542, A	C 492	13.6	68.0	67	4	US-09-814-351-12	Sequence 12, Appl
C 420	13.8	69.0	57280	4	US-09-949-016-13543	Sequence 13543, A	C 493	13.6	68.0	135	4	US-09-513-999C-14516	Sequence 14516, A
C 421	13.8	69.0	57280	4	US-09-949-016-13544	Sequence 13544, A	C 494	13.6	68.0	137	4	US-09-513-999C-27272	Sequence 27272, A
C 422	13.8	69.0	57280	4	US-09-949-016-13545	Sequence 13545, A	C 495	13.6	68.0	166	4	US-09-513-999C-32611	Sequence 32611, A
C 423	13.8	69.0	57280	4	US-09-949-016-14633	Sequence 14633, A	C 496	13.6	68.0	226	4	US-09-513-999C-23309	Sequence 23309, A
C 424	13.8	69.0	57280	4	US-09-949-016-14634	Sequence 14634, A	C 497	13.6	68.0	253	4	US-09-513-999C-14344	Sequence 14344, A
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C 426	13.8	69.0	57280	4	US-09-949-016-14636	Sequence 14636, A	C 499	13.6	68.0	290	3	US-09-280-116-129	Sequence 129, App
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C 428	13.8	69.0	57280	4	US-09-949-016-14638	Sequence 14638, A							
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C 430	13.8	69.0	57280	4	US-09-949-016-14640	Sequence 14640, A							
C 431	13.8	69.0	68283	4	US-09-949-016-12261	Sequence 12261, A							
C 432	13.8	69.0	68444	4	US-09-949-016-13968	Sequence 13968, A							
C 433	13.8	69.0	68702	4	US-09-949-016-16328	Sequence 16328, A							
C 434	13.8	69.0	70000	3	US-09-851-896-3	Sequence 3, Appl							
C 435	13.8	69.0	76221	4	US-09-949-016-17009	Sequence 12009, A							
C 436	13.8	69.0	76221	4	US-09-949-016-17053	Sequence 17053, A							
C 437	13.8	69.0	76399	4	US-09-949-016-16619	Sequence 16619, A							
C 438	13.8	69.0	84495	3	US-09-797-906-3	Sequence 3, Appl							
C 439	13.8	69.0	85869	4	US-09-949-016-12017	Sequence 12017, A							
C 440	13.8	69.0	85878	4	US-09-949-016-16321	Sequence 16321, A							
C 441	13.8	69.0	87190	4	US-09-949-016-16335	Sequence 16335, A							
C 442	13.8	69.0	88906	4	US-09-949-016-17468	Sequence 17468, A							
C 443	13.8	69.0	93510	4	US-09-949-016-15095	Sequence 15095, A							
C 444	13.8	69.0	100463	4	US-09-949-016-12511	Sequence 12511, A							
C 445	13.8	69.0	100468	4	US-09-949-016-13725	Sequence 13725, A							
C 446	13.8	69.0	109159	4	US-09-949-016-14169	Sequence 14169, A							
C 447	13.8	69.0	109159	4	US-09-949-016-14170	Sequence 14170, A							
C 448	13.8	69.0	117937	4	US-09-949-016-12762	Sequence 12762, A							
C 449	13.8	69.0	117937	4	US-09-949-016-15775	Sequence 15775, A							
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C 451	13.8	69.0	118382	4	US-09-949-016-15997	Sequence 15997, A							
C 452	13.8	69.0	121068	4	US-09-949-016-14138	Sequence 14138, A							
C 453	13.8	69.0	126468	4	US-09-949-016-14418	Sequence 14418, A							
C 454	13.8	69.0	131724	4	US-09-949-016-12893	Sequence 12893, A							
C 455	13.8	69.0	175265	4	US-09-949-016-16089	Sequence 16089, A							
C 456	13.8	69.0	197336	4	US-09-949-016-12881	Sequence 12881, A							
C 457	13.8	69.0	197337	4	US-09-949-016-14376	Sequence 14376, A							
C 458	13.8	69.0	234288	4	US-09-949-016-17272	Sequence 17272, A							
C 459	13.8	69.0	251672	4	US-09-949-016-17296	Sequence 17296, A							
C 460	13.8	69.0	251682	4	US-09-949-016-11973	Sequence 11973, A							
C 461	13.8	69.0	251769	4	US-09-949-016-13185	Sequence 13185, A							
C 462	13.8	69.0	251769	4	US-09-949-016-13186	Sequence 13186, A							
C 463	13.8	69.0	266748	4	US-09-949-016-13187	Sequence 13187, A							
C 464	13.8	69.0	266748	4	US-09-949-016-13188	Sequence 13188, A							
C 465	13.8	69.0	392000	4	US-10-027-983-11	Sequence 11, Appl							

ALIGNMENTS

RESULT 1

US-09-949-016-5659/c

Sequence 5659, Application US/09949016

Patent No 6812319

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-08-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5659

LENGTH: 2087

TYPE: DNA

ORGANISM: Human

US-09-949-016-5659

Query Match

Best Local Similarity

Matches

100.0%;

Score 20;

DB 4;

Length 2087;

100.0%;

Pred. No. 1.5;

0;

Mismatches

0;

Indels

0;

Gaps

0;

QY

1

ACGGCGTCTCTAGTAGCAG

20

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1134

AGGGCGTCTCTAGTAGCAG

1115

Db

1134

AGGGCGTCTCTAGTAGCAG

1115

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RESULT 2
US-08-635-552A-1/c
; Sequence 1, Application US/08635552A
; Patent No. 6423514
; GENERAL INFORMATION:
; APPLICANT: Briskin, Michael J.
; TITLE OF INVENTION: Mammalian Hyaluronan Synthases, Nucleic
; TITLE OF INVENTION: Acids and Uses Thereof
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/635.552A
; FILING DATE: 22-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: LKS95-07
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2116 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 36..1769
US-08-635-552A-1

Query Match 100.0%; Score 20; DB 3; Length 2116;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGCGTCTCTGAGTAGCAG 20
Db 1134 AGGGCGTCTCTGAGTAGCAG 1115

RESULT 3
US-09-155-768-1/c
; Sequence 1, Application US/09155768A
; Patent No. 6162908
; GENERAL INFORMATION:
; APPLICANT: SEIKAGAKU CORPORATION
; TITLE OF INVENTION: POLYPEPTIDE OF HYALURONAN SYNTHASE OF
; TITLE OF INVENTION: HUMAN-ORIGIN AND DNA ENCODING THE SAME
; FILE REFERENCE: TOYAM37 001APC
; CURRENT APPLICATION NUMBER: US/09/155,768A
; CURRENT FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: JP 8-084326
; EARLIER FILING DATE: 1996-04-05
; EARLIER APPLICATION NUMBER: JP 8-109663
; EARLIER FILING DATE: 1996-04-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2117

Query Match 100.0%; Score 20; DB 3; Length 2117;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGCGTCTCTGAGTAGCAG 20
Db 1134 AGGGCGTCTCTGAGTAGCAG 1115

RESULT 4
US-09-949-016-17401/c
; Sequence 17401, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17401
; LENGTH: 14862
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17401

Query Match 100.0%; Score 20; DB 4; Length 14862;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGCGTCTCTGAGTAGCAG 20
Db 11909 AGGGCGTCTCTGAGTAGCAG 11890

RESULT 5
US-09-513-999C-14085
; Sequence 14085, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 14085
; LENGTH: 278
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-14085
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Query Match 84.0%; Score 16.8; DB 4; Length 278;
Best Local Similarity 90.0%; Pred. No. 48;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
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Db 113 AGGGCATCTCTGAGTTGCAG 132

RESULT 6
US-09-513-999C-2290
; Sequence 2290, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 2290
; LENGTH: 313
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 103..312
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 146
; OTHER INFORMATION: y=c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 169
; OTHER INFORMATION: w=a or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 284
; OTHER INFORMATION: w=a or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 267
; OTHER INFORMATION: k=g or t
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 15
; OTHER INFORMATION: Xaa=Leu or Pro
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 23
; OTHER INFORMATION: Xaa=Ser or Thr
US-09-513-999C-2290

Query Match 84.0%; Score 16.8; DB 4; Length 313;
Best Local Similarity 90.0%; Pred. No. 48;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
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Db 113 AGGGCATCTCTGAGTTGCAG 132

RESULT 7
US-09-904-196B-2
; Sequence 2, Application US/09904196B
; Patent No. 6555660
; GENERAL INFORMATION:

; APPLICANT: NISSEN, TORBEN LAUESGAARD
; APPLICANT: ANDERSEN, KIM VILBOUR
; APPLICANT: HANSEN, CHRISTIAN KARSTEN
; APPLICANT: MIKKELSEN, JAN MOLLER
; TITLE OF INVENTION: G-CSF CONJUGATES
; FILE REFERENCE: 31-000700US
; CURRENT APPLICATION NUMBER: US/09/904,196B
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US/09/760,008
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/176,376
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/189,506
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/215,644
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DK PA 2000 00024
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: DK PA 2000 00341
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: DK PA 2000 00943
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-904-196B-2

Query Match 79.0%; Score 15.8; DB 4; Length 525;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGTCTCTGAGTAGCAG 20
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Db 173 GGGCGCTCTGAGTAGCTG 191

RESULT 8
US-09-760-008A-2
; Sequence 2, Application US/09760008A
; Patent No. 6646110
; GENERAL INFORMATION:
; APPLICANT: NISSEN, TORBEN LAUESGAARD
; APPLICANT: ANDERSEN, KIM VILBOUR
; APPLICANT: HANSEN, CHRISTIAN KARSTEN
; APPLICANT: MIKKELSEN, JAN MOLLER
; TITLE OF INVENTION: G-CSF CONJUGATES
; FILE REFERENCE: 31-000700US
; CURRENT APPLICATION NUMBER: US/09/760,008A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/176,376
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/189,506
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/215,644
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DK PA 2000 00024
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: DK PA 2000 00341
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: DK PA 2000 00943
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-760-008A-2

Query Match 79.0%; Score 15.8; DB 4; Length 525;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGTCTCTGAGTAGCAG 20
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DB 173 GGGCGCTCTGAGTAGCTG 191

RESULT 9

US-10-192-294-2
; Sequence 2, Application US/10192294
; Patent No. 6811158
; GENERAL INFORMATION:
; APPLICANT: NISSEN, Torben Lauesgaard
; TITLE OF INVENTION: G-CSF Conjugates
; FILE REFERENCE: 0258us310
; CURRENT APPLICATION NUMBER: US/10/192,294
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 09/904,196
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: DK PA 2002 00447
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: DK PA 2002 00708
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: DNA sequence encoding hG-CSF, with codon usage for E. coli
US-10-192-294-2

Query Match 79.0%; Score 15.8; DB 4; Length 525;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGTCTCTGAGTAGCAG 20
|||||
DB 173 GGGCGCTCTGAGTAGCTG 191

RESULT 10

US-09-949-016-62651
; Sequence 62651, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62651
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-62651

Query Match 79.0%; Score 15.8; DB 4; Length 601;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGTCTCTGAGTAGCAG 20
|||||
DB 533 GGGCGCTCTCTGAGGAGCAG 551

RESULT 11

US-09-949-016-62652
; Sequence 62652, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62652
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-62652

Query Match 79.0%; Score 15.8; DB 4; Length 601;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGTCTCTGAGTAGCAG 20
|||||
DB 394 GGGCGCTCTCTGAGGAGCAG 412

RESULT 12

US-09-949-016-62687
; Sequence 62687, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62687
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-62687

Query Match 79.0%; Score 15.8; DB 4; Length 601;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGTCTCTGAGTAGCAG 20

Db 533 GGGCGTCTCTGAGGACGAG 551
||||| ||||| ||||| |||||

RESULT 13

US-09-949-016-62688
; Sequence 88844, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62688
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-62688

Query Match 79.0%; Score 15.8; DB 4; Length 601;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGTCTCTGAGTAGCAG 20
||||| ||||| ||||| |||||

Db 394 GGGCGTCTCTGAGGACGAG 412

RESULT 14

US-09-949-016-88843
; Sequence 88843, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88843
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-88843

Query Match 79.0%; Score 15.8; DB 4; Length 601;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGTCTCTGAGTAGCAG 20

Db 357 GGGCGTCTCTGAGGACGAG 375
||||| ||||| ||||| |||||

RESULT 15

US-09-949-016-88844
; Sequence 88844, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88844
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-88844

Query Match 79.0%; Score 15.8; DB 4; Length 601;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGTCTCTGAGTAGCAG 20
||||| ||||| ||||| |||||

Db 376 GGGCGTCTCTGATGAGCAG 394

RESULT 16

US-09-252-991A-10864/c
; Sequence 10864, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 10864
; LENGTH: 882
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-10864

Query Match 79.0%; Score 15.8; DB 4; Length 882;
Best Local Similarity 89.5%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGTCTCTGAGTAGCAG 20
||||| ||||| ||||| |||||

Db 177 GGGCGTCTCGGCTAGCAG 159

RESULT 17

US-09-902-540-5986/c
; Sequence 5986, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.

1. **Introduction**

GENERAL INFORMATION:
; APPLICANT: Lee, Mu-En
; TITLE OF INVENTION: SINGLE GENE ENCODING AORTIC-SPECIFIC AND STRIATED-SPECIFIC
; FILE REFERENCE: 05433/039001
; CURRENT APPLICATION NUMBER: US/09/303,069A
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: US 09/134,250
; EARLIER FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 2614
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)....(1806)
US-09-303-069-15

Query Match 79.0%; Score 15.8; DB 3; Length 2614;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGTCTCTGAGTAGCAG 20
DB 1273 GGGCGTCTCTGAGTAGCAG 1255

RESULT 22
US-09-134-250-15/c
; Sequence 15, Application US/09134250B
; Patent No. 6399753
; GENERAL INFORMATION:
; APPLICANT: Lee, Mu-En
; TITLE OF INVENTION: SINGLE GENE ENCODING AORTIC-SPECIFIC AND STRIATED-SPECIFIC
; FILE REFERENCE: 05433/038001
; CURRENT APPLICATION NUMBER: US/09/134,250B
; CURRENT FILING DATE: 1998-08-14
; EARLIER APPLICATION NUMBER: US 08/795,868
; EARLIER FILING DATE: 1997-02-06
; EARLIER APPLICATION NUMBER: US 08/494,577
; EARLIER FILING DATE: 1995-06-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 2614
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)....(1806)
US-09-134-250-15

Query Match 79.0%; Score 15.8; DB 3; Length 2614;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGTCTCTGAGTAGCAG 20
DB 1273 GGGCGTCTCTGAGTAGCAG 1255

RESULT 23
US-09-791-105B-1/c
; Sequence 1, Application US/09791105B
; Patent No. 6723508
; GENERAL INFORMATION:
; APPLICANT: EPIDAUROS Biotechnologie AG
; TITLE OF INVENTION: Method for detecting the presence of at least one single allele d

GENERAL INFORMATION:
; FILE REFERENCE: US 09,791,105
; CURRENT APPLICATION NUMBER: US/09/791,105B
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: EP20000103844 20000224
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-791-105B-1

Query Match 79.0%; Score 15.8; DB 4; Length 5000;
Best Local Similarity 89.5%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGTCTCTGAGTAGCAG 20
DB 3623 GGGCGTCTCTGAGTAGCAG 3605

RESULT 24
US-09-949-016-12503/c
; Sequence 12503, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12503
; LENGTH: 37792
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12503

Query Match 79.0%; Score 15.8; DB 4; Length 37792;
Best Local Similarity 89.5%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGTCTCTGAGTAGCAG 20
DB 13159 GGGCGTCTCTGAGTAGCAG 13141

RESULT 25
US-09-949-016-14263/c
; Sequence 14263, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

```
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14263
; LENGTH: 37795
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14263

Query Match          79.0%; Score 15.8; DB 4; Length 37795;
Best Local Similarity 89.5%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGCGTCTCTGAGTAGCAG 20
Db 13159 GGGCGTCTCTGAGTAGCAG 13141

RESULT 26
US-09-949-016-13547
; Sequence 13547, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13547
; LENGTH: 46085
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc feature
; LOCATION: (1)...(46085)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13547

Query Match          79.0%; Score 15.8; DB 4; Length 46085;
Best Local Similarity 89.5%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGCGTCTCTGAGTAGCAG 20
Db 4900 GGGCGTCTCTGAGTAGCAG 4918

RESULT 27
US-09-949-016-13548
; Sequence 13548, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
```

```
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13548
; LENGTH: 46085
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(46085)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13548

Query Match          79.0%; Score 15.8; DB 4; Length 46085;
Best Local Similarity 89.5%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGCGTCTCTGAGTAGCAG 20
Db 4900 GGGCGTCTCTGAGTAGCAG 4918

RESULT 28
US-10-148-806-3
; Sequence 3, Application US/10148806
; Patent No. 6762042
; GENERAL INFORMATION:
; APPLICANT: Bai, Chang
; APPLICANT: Metzger, Michael
; APPLICANT: Liu, Xiaomei
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NHL, A DNA
; FILE REFERENCE: 20585P
; CURRENT APPLICATION NUMBER: US/10/148,806
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US00/33065
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: 60/169,970
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 114793
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-148-806-3

Query Match          79.0%; Score 15.8; DB 4; Length 114793;
Best Local Similarity 89.5%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGCGTCTCTGAGTAGCAG 20
Db 49994 GGGCGTCTCTGAGTAGCAG 50012

RESULT 29
US-09-791-105B-32/C
; Sequence 32, Application US/09791105B
; Patent No. 6723508
; GENERAL INFORMATION:
; APPLICANT: EPIDAUROS Biotechnologie AG
; TITLE OF INVENTION: Method for detecting the presence of at least one single allele of
; FILE REFERENCE: US 09/791,105
; CURRENT APPLICATION NUMBER: US/09/791,105B
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: EP20000103844 20000224
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 118999
; TYPE: DNA
```

```

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(118999)
; OTHER INFORMATION: Homo sapiens genomic DNA, chromosome 22q11.2, clone KB226F1, Genb
; OTHER INFORMATION: ank accession number AF000351.2 GI:5420485
US-09-791-105B-32

Query Match          79.0%; Score 15.8; DB 4; Length 118999;
Best Local Similarity 89.5%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGTCTCTGAGTAGCAG 20
    ||||| ||||| |||||
Db 110366 GGGCGTCTCTGAGGAGCAG 110348

RESULT 30
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match          79.0%; Score 15.8; DB 3; Length 4403765;
Best Local Similarity 89.5%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCA 19
    ||||| ||||| |||||
Db 495282 AGGGCGTCCATGAGTAGCA 495300

RESULT 31
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv

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```

US-09-103-840A-1

Query Match          79.0%; Score 15.8; DB 3; Length 4411529;
Best Local Similarity 89.5%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCA 19
    ||||| ||||| |||||
Db 493840 AGGGCGTCCATGAGTAGCA 493858

RESULT 32
US-09-949-016-12847
; Sequence 12847, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12847
; LENGTH: 40546
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12847

Query Match          77.0%; Score 15.4; DB 4; Length 40546;
Best Local Similarity 94.1%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGGCTCTCTGAGTAGCA 19
    ||||| ||||| |||||
Db 29363 GGGCTCTCTGAGTAGCA 29379

RESULT 33
US-09-949-016-12915
; Sequence 12915, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12915
; LENGTH: 40546
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12915

Query Match          77.0%; Score 15.4; DB 4; Length 40546;
Best Local Similarity 94.1%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 184
; OTHER INFORMATION: m=a or c
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 196
; OTHER INFORMATION: r=a or g
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 198
; OTHER INFORMATION: m=a or c
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 214
; OTHER INFORMATION: k=g or t
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 232
; OTHER INFORMATION: r=a or g
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 234
; OTHER INFORMATION: r=a or g
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 238
; OTHER INFORMATION: w=a or t
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 241
; OTHER INFORMATION: m=a or c
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 389
; OTHER INFORMATION: r=a or g
;
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 10
; OTHER INFORMATION: Xaa=Ala or Asp
;
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 15
; OTHER INFORMATION: Xaa=His or Gln
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; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 22
; OTHER INFORMATION: Xaa=Asp or Gly
;
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 74
; OTHER INFORMATION: Xaa=Ala or Thr
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US-09-513-999C-809
Query Match          76.0%; Score 15.2; DB 4; Length 499;
Best Local Similarity 85.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 AGGGCGTCTCTCAGTAGCAG 20
Db      84 AGGGCGTCTCTCAGTAGCAG 65

RESULT 38
US-09-270-767-1973
; Sequence 1973, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 1973
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5447
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-5447

Query Match          76.0%; Score 15.2; DB 4; Length 597;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 AGGGCGTCTCTCAGTAGCAG 20
Db      190 AGGGCAGCTCTCAGTAGCAG 171

RESULT 41
US-09-270-767-20729/c
; Sequence 5447, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5447
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-5447

Query Match          76.0%; Score 15.2; DB 4; Length 597;
Best Local Similarity 85.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 AGGGCGTCTCTCAGTAGCAG 20
Db      121 AGGGCGTCTCCGAGCAGCG 140

RESULT 39
US-09-270-767-17255
; Sequence 17255, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17255
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-17255

Query Match          76.0%; Score 15.2; DB 4; Length 526;
Best Local Similarity 85.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 AGGGCGTCTCTCAGTAGCAG 20
Db      121 AGGGCGTCTCCGAGCAGCG 140

RESULT 40
US-09-270-767-5447/c
; Sequence 5447, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5447
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-5447

Query Match          76.0%; Score 15.2; DB 4; Length 597;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 AGGGCGTCTCTCAGTAGCAG 20
Db      190 AGGGCAGCTCTCAGTAGCAG 171

RESULT 41
US-09-270-767-20729/c
; Sequence 5447, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5447
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-5447
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; Sequence 20729, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20729
; LENGTH: 597
; TYPE: DNA
; ORGANISM: *Drosophila melanogaster*
US-09-270-767-20729

Query Match 76.0%; Score 15.2; DB 4; Length 597;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
||||| ||||||| |||||
Db 190 AGGGCAGCTCTGAGCAGCAG 171

RESULT 42

US-09-949-016-122359/c
; Sequence 122359, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 122359
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-122359

Query Match 76.0%; Score 15.2; DB 4; Length 601;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
||||| ||||||| |||||
Db 377 AGGGCTACCTGAGTAGCAG 358

RESULT 43

US-09-949-016-122360/c
; Sequence 122360, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 122360
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-122360

Query Match 76.0%; Score 15.2; DB 4; Length 601;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
||||| ||||||| |||||
Db 345 AGGGCTACCTGAGTAGCAG 326

RESULT 44

US-09-949-016-167564/c
; Sequence 167564, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 167564
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-167564

Query Match 76.0%; Score 15.2; DB 4; Length 601;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
||||| ||||||| |||||
Db 532 ATGGAGTCTCAGAGTAGCAG 513

RESULT 45

US-09-949-016-167671/c
; Sequence 167671, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 167671
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-167671

Query Match 76.0%; Score 15.2; DB 4; Length 601;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGCGCTCTCTGAGTAGCAG 20
||| ||||| ||||| |||||
Db 532 ATGGAGTCTCAGAGTAGCAG 513

RESULT 46
US-09-252-991A-607
; Sequence 607, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 607
; LENGTH: 606
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-607

Query Match 76.0%; Score 15.2; DB 4; Length 606;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGCGCTCTCTGAGTAGCAG 20
||| ||||| ||||| |||||
Db 503 AGGCGCGCTGAGCAGCAG 522

RESULT 47
US-09-879-792-28/c
; Sequence 28, Application US/09879792
; Patent No. 6734006
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; APPLICANT: Gedrich, Richard
; TITLE OF INVENTION: Regulation of Human Transmembrane Serine
; TITLE OF INVENTION: Protease
; FILE REFERENCE: 02973.00035
; CURRENT APPLICATION NUMBER: US/09/879,792
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/211,224
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US 60/283,353
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/283,648
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: PCT (Docket No. 6734006 LIO-81-WO)
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 834
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-879-792-28

Query Match 76.0%; Score 15.2; DB 4; Length 834;
Best Local Similarity 85.0%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGCGCTCTCTGAGTAGCAG 20
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Db 119 AGGTCTTCTCTGAGTAGGAG 100

RESULT 48
US-09-902-540-8443/c
; Sequence 8443, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8443
; LENGTH: 1164
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-8443

Query Match 76.0%; Score 15.2; DB 4; Length 1164;
Best Local Similarity 85.0%; Pred. No. 3.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGCGCTCTCTGAGTAGCAG 20
||| ||||| ||||| |||||
Db 104 AGGCGCTCTGAGCAGCAG 85

RESULT 49
US-09-252-991A-520/c
; Sequence 520, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 520
; LENGTH: 1182
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-520

Query Match 76.0%; Score 15.2; DB 4; Length 1182;
Best Local Similarity 85.0%; Pred. No. 3.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGCGCTCTCTGAGTAGCAG 20
||| ||||| ||||| |||||
Db 200 AGGCGCGCTGAGCAGCAG 181

RESULT 50

US-09-270-767-29815
; Sequence 29815, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29815
; LENGTH: 1219
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-29815

Query Match 76.0%; Score 15.2; DB 4; Length 1219;
Best Local Similarity 85.0%; Pred. No. 3.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
Db 627 AGGGCGTCTCTGAGTAGCAG 646

Search completed: March 14, 2005, 20:48:00
Job time : 149 secs

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OM nucleic - nucleic search, using sw model

Run on: March 14, 2005, 20:46:15 ; Search time 328 Seconds
(without alignments)
362.715 Million cell updates/sec

Title: US-10-672-399-10

Perfect score: 20

Sequence: 1 agggcgctctgtagtagcag 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 11075104

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Published Applications NA:*

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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
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19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	18	US-10-672-399-10
2	20	100.0	1071	18	US-10-672-399-3
3	20	100.0	1083	18	US-10-672-399-5
4	20	100.0	1737	18	US-10-672-399-1
5	20	100.0	2116	13	US-10-042-523-1
6	17.4	87.0	1752	10	US-09-902-939-1
7	16.8	84.0	188	18	US-10-425-115-88239
8	16.8	84.0	239	16	US-10-029-386-22234
9	16.8	84.0	595	16	US-10-029-386-8534
10	16.8	84.0	80105	18	US-10-322-281-223
11	16.4	82.0	300	14	US-10-076-555-218
					Sequence 10, Appli
					Sequence 3, Appli
					Sequence 5, Appli
					Sequence 1, Appli
					Sequence 1, Appli
					Sequence 82339, A
					Sequence 22334, A
					Sequence 8534, Ap
					Sequence 223, App
					Sequence 218, App

12	16.4	82.0	452	14	US-10-076-555-842	Sequence 842, App
13	16.4	82.0	748	17	US-10-260-238-3940	Sequence 3940, Ap
14	16.4	82.0	1611	17	US-10-104-047-1094	Sequence 1094, Ap
15	16.4	82.0	1992	9	US-09-925-301-256	Sequence 256, App
16	16.4	82.0	2665	17	US-10-264-237-795	Sequence 795, App
17	16.4	82.0	4560	18	US-10-723-860-6203	Sequence 6203, Ap
18	15.8	79.0	458	10	US-09-918-995-2858	Sequence 2858, A
19	15.8	79.0	525	9	US-09-760-008A-2	Sequence 2, Appli
20	15.8	79.0	525	15	US-09-904-196B-2	Sequence 2, Appli
21	15.8	79.0	525	15	US-10-192-294-2	Sequence 2, Appli
22	15.8	79.0	525	16	US-10-318-966-2	Sequence 2, Appli
23	15.8	79.0	525	18	US-10-705-745-2	Sequence 2, Appli
24	15.8	79.0	531	13	US-10-003-496-5	Sequence 5, Appli
25	15.8	79.0	600	18	US-10-437-963-27903	Sequence 27903, A
26	15.8	79.0	874	13	US-10-027-632-142002	Sequence 142002, A
27	15.8	79.0	874	17	US-10-027-632-169596	Sequence 169596, A
28	15.8	79.0	874	17	US-10-027-632-142002	Sequence 142002, A
29	15.8	79.0	874	17	US-10-027-632-169596	Sequence 169596, A
30	15.8	79.0	1113	13	US-10-027-632-116504	Sequence 116504, A
31	15.8	79.0	1113	17	US-10-027-632-116504	Sequence 116504, A
32	15.8	79.0	1196	17	US-10-424-599-16815	Sequence 16815, A
33	15.8	79.0	1326	18	US-10-437-963-34349	Sequence 34349, A
34	15.8	79.0	1938	17	US-10-424-599-110517	Sequence 110517, A
35	15.8	79.0	2196	18	US-10-437-963-67253	Sequence 67253, A
36	15.8	79.0	2597	13	US-10-027-632-111979	Sequence 111979, A
37	15.8	79.0	2597	17	US-10-027-632-111979	Sequence 111979, A
38	15.8	79.0	2614	13	US-10-160-865-15	Sequence 15, Appli
39	15.8	79.0	5000	9	US-09-791-105-1	Sequence 1, Appli
40	15.8	79.0	5727	17	US-10-334-143-98	Sequence 98, Appli
41	15.8	79.0	5866	17	US-10-144-194A-87	Sequence 87, Appli
42	15.8	79.0	5866	18	US-10-491-566-87	Sequence 87, Appli
43	15.8	79.0	53795	11	US-09-997-722-124	Sequence 124, App
44	15.8	79.0	73465	18	US-10-450-826-68	Sequence 68, Appli
45	15.8	79.0	114793	15	US-10-148-806-3	Sequence 3, Appli
46	15.8	79.0	153170	18	US-10-723-860-199	Sequence 199, App
47	15.4	77.0	397	18	US-10-425-115-71771	Sequence 17771, A
48	15.4	77.0	431	18	US-10-653-047-1507	Sequence 1507, Ap
49	15.4	77.0	433	9	US-09-560-863-242	Sequence 242, App
50	15.4	77.0	488	9	US-09-783-590-10350	Sequence 10350, A
51	15.4	77.0	534	13	US-10-027-632-290561	Sequence 290561, A
52	15.4	77.0	534	17	US-10-027-632-290561	Sequence 290561, A
53	15.4	77.0	664	18	US-10-425-115-136834	Sequence 136834, A
54	15.4	77.0	796	13	US-10-027-632-143571	Sequence 143571, A
55	15.4	77.0	796	17	US-10-027-632-143571	Sequence 143571, A
56	15.4	77.0	1066	17	US-10-291-265-620	Sequence 620, App
57	15.4	77.0	1255	17	US-10-291-265-148	Sequence 148, App
58	15.4	77.0	1285	16	US-10-380-558-1	Sequence 1, Appli
59	15.4	77.0	1285	16	US-10-380-558-3	Sequence 3, Appli
60	15.4	77.0	156843	13	US-10-087-192-1408	Sequence 1408, Ap
61	15.2	76.0	21	18	US-10-802-441-12	Sequence 12, Appli
62	15.2	76.0	25	19	US-10-809-189-69161	Sequence 69161, A
63	15.2	76.0	128	17	US-10-424-599-102822	Sequence 102822, A
64	15.2	76.0	159	9	US-09-864-761-31331	Sequence 31331, A
65	15.2	76.0	187	17	US-10-424-599-92422	Sequence 92422, A
66	15.2	76.0	380	11	US-09-732-637A-2542	Sequence 2542, Ap
67	15.2	76.0	415	17	US-10-242-535A-41159	Sequence 41159, A
68	15.2	76.0	415	17	US-10-085-783A-41159	Sequence 41159, A
69	15.2	76.0	418	18	US-10-425-115-532	Sequence 532, App
70	15.2	76.0	461	18	US-10-767-701-6722	Sequence 6722, Ap
71	15.2	76.0	473	13	US-10-027-632-86867	Sequence 86867, A
72	15.2	76.0	473	13	US-10-027-632-303658	Sequence 303658, A
73	15.2	76.0	473	17	US-10-027-632-303658	Sequence 303658, A
74	15.2	76.0	473	17	US-10-027-632-303658	Sequence 303658, A
75	15.2	76.0	498	10	US-09-918-995-23748	Sequence 23748, A
76	15.2	76.0	503	10	US-09-918-995-20965	Sequence 20965, A
77	15.2	76.0	548	17	US-10-291-172-380	Sequence 380, App
78	15.2	76.0	548	17	US-10-221-278-380	Sequence 380, App
79	15.2	76.0	554	9	US-09-864-761-14834	Sequence 14834, A
80	15.2	76.0	645	13	US-10-027-632-127748	Sequence 127748, A
81	15.2	76.0	645	13	US-10-027-632-127748	Sequence 127748, A
82	15.2	76.0	645	13	US-10-027-632-127750	Sequence 127750, A
83	15.2	76.0	645	13	US-10-027-632-127751	Sequence 127751, A
84	15.2	76.0	645	17	US-10-027-632-127748	Sequence 127748, A

C 85	15.2	76.0	645	17	US-10-027-632-127749	Sequence 127749,	158	15.2	76.0	1980090	18	US-10-719-993-6815	Sequence 6815, Ap
C 86	15.2	76.0	645	17	US-10-027-632-127750	Sequence 127750,	159	15.2	76.0	1980090	19	US-10-741-600-17676	Sequence 17676, A
C 87	15.2	76.0	645	17	US-10-027-632-127751	Sequence 127751,	160	15	75.0	456	10	US-09-918-995-20598	Sequence 20598, A
C 88	15.2	76.0	684	10	US-09-972-656-83	Sequence 83, Appl	161	15	75.0	552	16	US-10-029-386-11879	Sequence 11879, A
C 89	15.2	76.0	741	18	US-10-437-963-822	Sequence 822, App	162	15	75.0	1379	17	US-10-291-265-36	Sequence 36, Appl
C 90	15.2	76.0	834	9	US-09-979-792-28	Sequence 28, Appl	163	15	75.0	11876	18	US-10-723-860-1800	Sequence 1800, Ap
C 91	15.2	76.0	834	18	US-10-806-370-28	Sequence 28, Appl	164	15	75.0	11919	18	US-10-723-860-6158	Sequence 6158, Ap
C 92	15.2	76.0	842	18	US-10-425-115-158723	Sequence 158723,	165	15	75.0	65464	9	US-09-859-888-3	Sequence 3, Appli
C 93	15.2	76.0	995	13	US-10-021-509-4	Sequence 4, Appli	166	15	75.0	65464	18	US-10-476-543-3	Sequence 3, Appli
C 94	15.2	76.0	995	13	US-10-021-509-12	Sequence 12, Appl	167	15	75.0	200418	13	US-10-087-132-568	Sequence 568, App
C 95	15.2	76.0	996	18	US-10-425-115-96589	Sequence 96589, A	168	14.8	74.0	25	19	US-10-719-900-462907	Sequence 462907,
C 96	15.2	76.0	1078	17	US-09-898-837A-16	Sequence 16, Appl	169	14.8	74.0	261	17	US-10-424-599-67106	Sequence 67106, A
C 97	15.2	76.0	1101	17	US-10-428-275-109	Sequence 109, App	170	14.8	74.0	295	9	US-09-784-423-8	Sequence 8, Appli
C 98	15.2	76.0	1110	17	US-10-428-275-113	Sequence 113, App	171	14.8	74.0	323	18	US-10-425-115-118330	Sequence 118330,
C 99	15.2	76.0	1146	17	US-10-428-275-133	Sequence 133, App	172	14.8	74.0	323	18	US-10-437-963-50208	Sequence 50208, A
C 100	15.2	76.0	1203	17	US-10-428-275-111	Sequence 111, App	173	14.8	74.0	376	17	US-10-424-599-26657	Sequence 26657, A
C 101	15.2	76.0	1203	17	US-10-428-275-115	Sequence 115, App	174	14.8	74.0	411	18	US-09-918-995-4283	Sequence 4283, Ap
C 102	15.2	76.0	1203	17	US-10-428-275-117	Sequence 117, App	175	14.8	74.0	422	18	US-10-914-016-121	Sequence 121, App
C 103	15.2	76.0	1218	17	US-10-428-275-125	Sequence 125, App	176	14.8	74.0	455	10	US-09-918-995-27588	Sequence 27588, A
C 104	15.2	76.0	1218	17	US-10-428-275-137	Sequence 137, App	177	14.8	74.0	467	9	US-09-864-761-1521	Sequence 1521, Ap
C 105	15.2	76.0	1230	9	US-09-879-792-35	Sequence 35, Appl	178	14.8	74.0	526	13	US-10-027-632-274696	Sequence 274696,
C 106	15.2	76.0	1230	18	US-10-806-370-35	Sequence 35, Appl	179	14.8	74.0	526	17	US-10-027-632-274696	Sequence 274696,
C 107	15.2	76.0	1314	10	US-09-898-837A-14	Sequence 14, Appl	180	14.8	74.0	547	17	US-10-424-599-70440	Sequence 70440, A
C 108	15.2	76.0	1314	10	US-09-898-837A-17	Sequence 17, Appl	181	14.8	74.0	552	18	US-10-335-053-245	Sequence 245, App
C 109	15.2	76.0	1314	17	US-10-428-275-131	Sequence 131, App	182	14.8	74.0	572	9	US-09-864-761-18280	Sequence 18280, A
C 110	15.2	76.0	1341	14	US-10-177-661-3	Sequence 3, Appli	183	14.8	74.0	646	13	US-10-027-632-122441	Sequence 122441,
C 111	15.2	76.0	1419	18	US-10-437-963-61831	Sequence 61831, A	184	14.8	74.0	646	17	US-10-027-632-122441	Sequence 122441,
C 112	15.2	76.0	1434	14	US-10-177-661-1	Sequence 1, Appli	185	14.8	74.0	707	17	US-10-260-238-3941	Sequence 3941, Ap
C 113	15.2	76.0	1574	17	US-10-274-639-29	Sequence 29, Appl	186	14.8	74.0	723	18	US-10-653-047-4658	Sequence 4658, Ap
C 114	15.2	76.0	1574	17	US-10-333-574-29	Sequence 29, Appl	187	14.8	74.0	731	18	US-10-437-963-41552	Sequence 41552, A
C 115	15.2	76.0	1589	18	US-10-425-115-101269	Sequence 101269,	188	14.8	74.0	785	17	US-10-260-238-4613	Sequence 4613, Ap
C 116	15.2	76.0	1614	9	US-09-888-615-45	Sequence 45, Appl	189	14.8	74.0	838	13	US-10-027-632-160660	Sequence 160660,
C 117	15.2	76.0	1626	17	US-10-428-275-121	Sequence 121, App	190	14.8	74.0	838	17	US-10-027-632-160660	Sequence 160660,
C 118	15.2	76.0	1626	18	US-10-425-115-86930	Sequence 86930, A	191	14.8	74.0	884	14	US-10-076-555-796	Sequence 796, App
C 119	15.2	76.0	1689	17	US-10-156-214A-23	Sequence 23, Appl	192	14.8	74.0	1158	10	US-09-372-348-28	Sequence 43, Appl
C 120	15.2	76.0	1707	17	US-10-428-275-129	Sequence 129, App	193	14.8	74.0	1168	9	US-09-778-844-43	Sequence 49, Appl
C 121	15.2	76.0	1708	17	US-10-428-275-147	Sequence 147, App	194	14.8	74.0	1254	10	US-09-825-476-49	Sequence 825, App
C 122	15.2	76.0	1748	9	US-09-879-792-11	Sequence 11, Appl	195	14.8	74.0	1414	18	US-10-437-963-825	Sequence 825, App
C 123	15.2	76.0	1748	18	US-10-806-370-11	Sequence 11, Appl	196	14.8	74.0	2271	15	US-10-259-165-149	Sequence 149, App
C 124	15.2	76.0	1771	17	US-10-428-275-123	Sequence 123, App	197	14.8	74.0	2346	17	US-10-062-674-4878	Sequence 1878, Ap
C 125	15.2	76.0	1779	17	US-10-428-275-119	Sequence 119, App	198	14.8	74.0	2455	18	US-10-425-115-148811	Sequence 148811,
C 126	15.2	76.0	2067	17	US-10-156-214A-25	Sequence 25, Appl	199	14.8	74.0	2484	17	US-10-108-260A-1543	Sequence 1543, Ap
C 127	15.2	76.0	2310	17	US-10-428-275-127	Sequence 127, App	200	14.8	74.0	2674	17	US-10-295-037-655	Sequence 655, App
C 128	15.2	76.0	2393	17	US-10-353-690-99	Sequence 99, Appl	201	14.8	74.0	2691	18	US-10-723-860-6540	Sequence 6540, Ap
C 129	15.2	76.0	2410	17	US-10-311-035-35	Sequence 35, Appl	202	14.8	74.0	2896	18	US-10-437-963-9614	Sequence 9614, Ap
C 130	15.2	76.0	2432	17	US-10-428-275-103	Sequence 103, App	203	14.8	74.0	3012	17	US-10-108-260A-1713	Sequence 1713, Ap
C 131	15.2	76.0	2432	17	US-10-428-275-139	Sequence 139, App	204	14.8	74.0	3396	18	US-10-793-639-530	Sequence 530, App
C 132	15.2	76.0	2432	17	US-10-428-275-141	Sequence 141, App	205	14.8	74.0	3589	18	US-10-478-914-21	Sequence 21, Appl
C 133	15.2	76.0	2432	17	US-10-428-275-143	Sequence 143, App	206	14.8	74.0	5912	10	US-09-825-476-1	Sequence 1, Appli
C 134	15.2	76.0	2643	9	US-09-350-874-56	Sequence 56, Appl	207	14.8	74.0	9171	9	US-09-810-993-1	Sequence 1, Appli
C 135	15.2	76.0	2643	13	US-10-106-989-56	Sequence 56, Appl	208	14.8	74.0	9171	10	US-09-825-476-2	Sequence 2, Appli
C 136	15.2	76.0	2717	13	US-10-027-632-111854	Sequence 111854,	209	14.8	74.0	9171	16	US-10-251-210-1	Sequence 1, Appli
C 137	15.2	76.0	2717	17	US-10-027-632-111854	Sequence 111854,	210	14.8	74.0	9196	8	US-08-984-090-1	Sequence 1, Appli
C 138	15.2	76.0	2727	17	US-10-291-172-4	Sequence 4, Appli	211	14.8	74.0	9196	15	US-10-361-562-1	Sequence 1, Appli
C 139	15.2	76.0	2727	17	US-10-221-278-4	Sequence 4, Appli	212	14.8	74.0	9385	14	US-10-175-225-1	Sequence 1, Appli
C 140	15.2	76.0	2772	16	US-10-119-428-4	Sequence 4, Appli	213	14.8	74.0	10948	15	US-10-017-161-2069	Sequence 2069, Ap
C 141	15.2	76.0	3678	18	US-10-425-114-13558	Sequence 13558, A	214	14.8	74.0	10948	17	US-10-292-798-1715	Sequence 1715, Ap
C 142	15.2	76.0	4859	18	US-10-425-115-118653	Sequence 118653,	215	14.8	74.0	17286	17	US-10-366-345-8	Sequence 8, Appli
C 143	15.2	76.0	5728	9	US-09-917-800A-479	Sequence 479, App	216	14.8	74.0	17286	18	US-10-723-860-2345	Sequence 7, Appli
C 144	15.2	76.0	5728	17	US-10-388-934-73	Sequence 73, Appl	217	14.8	74.0	21898	17	US-10-034-650-7	Sequence 7, Appli
C 145	15.2	76.0	7513	15	US-10-017-161-1779	Sequence 161, App	218	14.8	74.0	25543	13	US-10-087-192-805	Sequence 805, App
C 146	15.2	76.0	7513	17	US-10-292-798-1435	Sequence 1435, Ap	219	14.8	74.0	26345	13	US-10-087-192-1705	Sequence 1705, Ap
C 147	15.2	76.0	15515	9	US-09-822-860-3	Sequence 3, Appli	220	14.8	74.0	26345	13	US-10-087-192-1705	Sequence 1705, Ap
C 148	15.2	76.0	25083	11	US-09-997-722-121	Sequence 121, App	221	14.8	74.0	28350	17	US-10-085-117-169	Sequence 169, App
C 149	15.2	76.0	25231	10	US-09-764-891-5800	Sequence 5800, Ap	222	14.8	74.0	28350	17	US-09-800-631-96	Sequence 96, Appl
C 150	15.2	76.0	44377	17	US-10-085-117-40	Sequence 40, Appl	223	14.8	74.0	30310	9	US-10-293-783-96	Sequence 745, Appl
C 151	15.2	76.0	49914	18	US-10-322-281-299	Sequence 299, App	224	14.8	74.0	30310	15	US-10-388-263-745	Sequence 745, App
C 152	15.2	76.0	63248	13	US-10-087-192-1879	Sequence 1879, Ap	225	14.8	74.0	30310	17	US-10-087-192-2035	Sequence 2035, Ap
C 153	15.2	76.0	102145	18	US-10-331-053-53	Sequence 53, Appl	226	14.8	74.0	30554	13	US-10-087-192-2035	Sequence 307, App
C 154	15.2	76.0	109725	18	US-10-719-993-6868	Sequence 6868, Ap	227	14.8	74.0	34511	17	US-10-085-117-307	Sequence 91, Appl
C 155	15.2	76.0	120144	18	US-10-322-281-143	Sequence 143, App	228	14.8	74.0	35425	18	US-10-322-696-91	Sequence 127, App
C 156	15.2	76.0	150085	18	US-10-417-375-167	Sequence 167, App	229	14.8	74.0	36048	17	US-10-052-482-127	Sequence 49, Appl
C 157	15.2	76.0	173808	13	US-10-003-806-10	Sequence 10, Appl	230	14.8	74.0	36211	17	US-10-085-117-49	Sequence 49, Appl

c 231	14.8	74.0	37135	17	US-10-052-482-151	Sequence 151, App	c 304	14.4	72.0	456	18	US-10-357-930-524	Sequence 524, App
c 232	14.8	74.0	39924	13	US-10-087-192-1993	Sequence 1993, Ap	c 305	14.4	72.0	473	18	US-10-723-860-3375	Sequence 3375, Ap
c 233	14.8	74.0	41522	13	US-10-087-192-1741	Sequence 1741, Ap	c 306	14.4	72.0	505	10	US-09-918-995-20349	Sequence 20349, A
c 234	14.8	74.0	42179	13	US-10-087-192-1969	Sequence 1969, Ap	c 307	14.4	72.0	560	17	US-10-152-319A-370	Sequence 370, App
c 235	14.8	74.0	42339	13	US-10-087-192-991	Sequence 991, App	c 308	14.4	72.0	589	13	US-10-027-632-135590	Sequence 135590,
c 236	14.8	74.0	44990	17	US-10-052-482-217	Sequence 217, App	c 309	14.4	72.0	589	17	US-10-027-632-135590	Sequence 135590,
c 237	14.8	74.0	45315	18	US-10-322-281-785	Sequence 785, App	c 310	14.4	72.0	593	16	US-10-029-386-4162	Sequence 4162, Ap
c 238	14.8	74.0	45606	17	US-10-085-117-253	Sequence 253, App	c 311	14.4	72.0	644	13	US-10-027-632-239018	Sequence 239018,
c 239	14.8	74.0	46137	18	US-10-322-281-353	Sequence 353, App	c 312	14.4	72.0	644	13	US-10-027-632-239018	Sequence 239018,
c 240	14.8	74.0	46137	18	US-10-322-281-353	Sequence 353, App	c 313	14.4	72.0	644	17	US-10-027-632-239018	Sequence 239018,
c 241	14.8	74.0	49502	13	US-10-087-192-1099	Sequence 1099, Ap	c 314	14.4	72.0	644	17	US-10-027-632-239019	Sequence 239019,
c 242	14.8	74.0	52312	18	US-10-322-281-753	Sequence 753, App	c 315	14.4	72.0	665	13	US-10-027-632-198234	Sequence 198234,
c 243	14.8	74.0	52637	18	US-10-367-094-186	Sequence 186, App	c 316	14.4	72.0	665	17	US-10-027-632-198234	Sequence 198234,
c 244	14.8	74.0	54810	18	US-10-417-375-91	Sequence 91, Appl	c 317	14.4	72.0	716	18	US-10-425-115-58096	Sequence 58096, A
c 245	14.8	74.0	55606	17	US-10-085-117-133	Sequence 133, App	c 318	14.4	72.0	756	13	US-10-027-632-147299	Sequence 147299,
c 246	14.8	74.0	62278	18	US-10-322-281-849	Sequence 849, App	c 319	14.4	72.0	756	13	US-10-027-632-147299	Sequence 147299,
c 247	14.8	74.0	65787	17	US-10-052-482-109	Sequence 109, App	c 320	14.4	72.0	756	17	US-10-027-632-147299	Sequence 147299,
c 248	14.8	74.0	66881	18	US-10-322-281-411	Sequence 411, App	c 321	14.4	72.0	756	17	US-10-027-632-147300	Sequence 147300,
c 249	14.8	74.0	67191	11	US-09-997-722-169	Sequence 169, App	c 322	14.4	72.0	759	9	US-09-822-849A-546	Sequence 546, App
c 250	14.8	74.0	67191	16	US-10-105-612-1	Sequence 1, Appli	c 323	14.4	72.0	779	18	US-10-425-115-58094	Sequence 58094, A
c 251	14.8	74.0	68233	17	US-10-034-650-31	Sequence 31, Appl	c 324	14.4	72.0	790	18	US-10-425-115-58094	Sequence 58094, A
c 252	14.8	74.0	73900	17	US-10-085-117-295	Sequence 295, App	c 325	14.4	72.0	872	19	US-10-487-561-19	Sequence 19, Appl
c 253	14.8	74.0	76150	17	US-10-085-117-157	Sequence 157, App	c 326	14.4	72.0	970	18	US-10-723-860-7358	Sequence 7358, Ap
c 254	14.8	74.0	80423	18	US-10-367-094-41	Sequence 41, Appl	c 327	14.4	72.0	987	10	US-09-944-049-11	Sequence 11, Appl
c 255	14.8	74.0	80767	17	US-10-085-117-97	Sequence 97, Appl	c 328	14.4	72.0	987	13	US-10-061-943A-4	Sequence 4, Appli
c 256	14.8	74.0	87415	13	US-10-087-192-1651	Sequence 1651, Ap	c 329	14.4	72.0	1058	9	US-09-864-761-16865	Sequence 16865, A
c 257	14.8	74.0	87464	13	US-10-087-192-1411	Sequence 1411, Ap	c 330	14.4	72.0	1058	13	US-10-108-605-140	Sequence 140, App
c 258	14.8	74.0	90043	13	US-10-087-192-1141	Sequence 1141, Ap	c 331	14.4	72.0	1419	13	US-10-108-605-140	Sequence 140, App
c 259	14.8	74.0	90351	18	US-10-367-094-166	Sequence 166, App	c 332	14.4	72.0	1601	10	US-09-960-706-465	Sequence 465, App
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c 262	14.8	74.0	96597	17	US-10-052-482-226	Sequence 226, App	c 335	14.4	72.0	1672	18	US-10-370-715B-129	Sequence 129, App
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ALIGNMENTS

RESULT 1

US-10-672-399-10

; Sequence 10, Application US/10672399

; Publication No. US20050003368A1

; GENERAL INFORMATION:

; APPLICANT: University of Alberta

; TITLE OF INVENTION: Cancer Monitoring and Therapeutics

; FILE REFERENCE: A894635US

; CURRENT APPLICATION NUMBER: US/10/672,399

; CURRENT FILING DATE: 2003-09-25

; PRIOR APPLICATION NUMBER: US 60/472,401

; PRIOR FILING DATE: 2003-05-22

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 10

; LENGTH: 20

; TYPE: DNA

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; Sequence 3, Application US/10672399
; Publication No. US20050003368A1
; GENERAL INFORMATION:
; APPLICANT: University of Alberta
; TITLE OF INVENTION: Cancer Monitoring and Therapeutics
; FILE REFERENCE: A894635US
; CURRENT APPLICATION NUMBER: US/10/672,399
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: US 60/472,401
; PRIOR FILING DATE: 2003-05-22
; NUMBER OF SEQ ID NOS: 14
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US-10-672-399-3
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; Publication No. US20050003368A1
; GENERAL INFORMATION:
; APPLICANT: University of Alberta
; TITLE OF INVENTION: Cancer Monitoring and Therapeutics
; FILE REFERENCE: A894635US
; CURRENT APPLICATION NUMBER: US/10/672,399
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: US 60/472,401
; PRIOR FILING DATE: 2003-05-22
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
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US-10-672-399-5
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RESULT 4
US-10-672-399-1/c
; Sequence 1, Application US/10672399
; Publication No. US20050003368A1
; GENERAL INFORMATION:
; APPLICANT: University of Alberta
; TITLE OF INVENTION: Cancer Monitoring and Therapeutics
; FILE REFERENCE: A894635US
; CURRENT APPLICATION NUMBER: US/10/672,399
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: US 60/472,401
; PRIOR FILING DATE: 2003-05-22
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1737
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-672-399-1
    Query Match      100.0%; Score 20; DB 18; Length 1737;
    Best Local Similarity 100.0%; Pred. No. 1.2; Indels 0; Gaps 0;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGGCGTCTCTGAGTAGCAG 20
    |||||
Db 1099 AGGGCGTCTCTGAGTAGCAG 1080
    |||||

RESULT 5
US-10-042-523-1/c
; Sequence 1, Application US/10042523
; Publication No. US20020151026A1
; GENERAL INFORMATION:
; APPLICANT: Briskin, Michael J.
; TITLE OF INVENTION: Mammalian Hyaluronan Synthases, Nucleic
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/042,523
; FILING DATE: 19-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/635,552A
; FILING DATE: 22-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: LKS95-07
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2116 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 36..1769
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-042-523-1
```

Query Match 100.0%; Score 20; DB 13; Length 2116;
Best Local Similarity 100.0%; Pred. No. 1.2; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCGCTCTCTGAGTAGCAG 20
|||||
DB 1134 AGGCGCTCTCTGAGTAGCAG 1115

RESULT 6

US-09-902-939-1/c
; Sequence 1, Application US/09902939
; Publication No. US20030087850A1
; GENERAL INFORMATION:
; APPLICANT: Philip DeHaza
; APPLICANT: William Chen
; TITLE OF INVENTION: GENE THERAPY FOR DRY EYE SYNDROME
; FILE REFERENCE: 2055/OH020-US0
; CURRENT APPLICATION NUMBER: US/09/902,939
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1752
; TYPE: DNA
; ORGANISM: mouse
US-09-902-939-1

Query Match 87.0%; Score 17.4; DB 10; Length 1752;
Best Local Similarity 94.7%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGCGCTCTCTGAGTAGCA 19
|||||
DB 1114 AGGCGCTCTCCGAGTAGCA 1096

RESULT 7

US-10-425-115-88239
; Sequence 88239, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 88239
; LENGTH: 188
; TYPE: DNA
; ORGANISM: zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(188)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_180473C.1
US-10-425-115-88239

Query Match 84.0%; Score 16.8; DB 18; Length 188;
Best Local Similarity 90.8%; Pred. No. 63;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGCGCTCTCTGAGTAGCAG 20
|||||
DB 99 ATGCGCTTCTGAGTAGCAG 118

RESULT 8

US-10-029-386-22234/c
; Sequence 22234, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 22234
; LENGTH: 239
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR19.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EST HUMAN HIT: BG618999.1, EVALUE 4.00e-47
; OTHER INFORMATION: SWISSPROT HIT: P01026, EVALUE 3.90e+00
; OTHER INFORMATION: NT HIT: gill1425973, EVALUE 0.00e+00
US-10-029-386-22234

Query Match 84.0%; Score 16.8; DB 16; Length 239;
Best Local Similarity 90.0%; Pred. No. 63;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGCGCTCTCTGAGTAGCAG 20
|||||
DB 113 AGGCATCTCTGAGTTGCAG 94

RESULT 9

US-10-029-386-8534/c
; Sequence 8534, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 8534
; LENGTH: 595
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR19.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
; OTHER INFORMATION: SWISSPROT HIT: Q9TC96, EVALUE 1.10e+00
; OTHER INFORMATION: NT HIT: gill1425973, EVALUE 0.00e+00
; OTHER INFORMATION: EST_HUMAN HIT: BF368912.1, EVALUE 8.00e-66
US-10-029-386-8534

Query Match 84.0%; Score 16.8; DB 16; Length 595;
Best Local Similarity 90.0%; Pred. No. 60;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGCGCTCTCTGAGTAGCAG 20
|||||
DB 422 AGGCATCTCTGAGTTGCAG 403

RESULT 10

US-10-322-281-223
; Sequence 223, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 223
; LENGTH: 80105
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(80105)
; OTHER INFORMATION: n = A,T,C or G
US-10-322-281-223

Query Match 84.0%; Score 16.8; DB 18; Length 80105;
Best Local Similarity 90.0%; Pred. No. 47;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGGCTCTCTGAGTAGCAG 20

Db 32700 AGGGTACTCTGAGTAGCAG 32719

RESULT 11

US-10-076-555-218
; Sequence 218, Application US/10076555
; Publication No. US20030065156A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Lewis T.
; APPLICANT: Escobedo, Jaime
; APPLICANT: Innis, Michael A.
; APPLICANT: Garcia, Pablo Dominiguez
; APPLICANT: Sudduth-Klinger, Julie
; APPLICANT: Reinhard, Christoph
; APPLICANT: Giese, Klaus
; APPLICANT: Randazzo, Filippo
; APPLICANT: Kennedy, Giulia C.
; APPLICANT: Pot, David
; APPLICANT: Kassam, Altaf
; APPLICANT: Lamson, George
; APPLICANT: Drmanac, Radoje
; APPLICANT: Crkvenjakov, Radomir
; APPLICANT: Dickson, Mark
; APPLICANT: Drmanac, Snezana
; APPLICANT: Labat, Ivan
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Kita, David
; APPLICANT: Garcia, Veronica
; APPLICANT: Jones, Lee William
; APPLICANT: Stache-Crain, Birgit
; TITLE OF INVENTION: Novel Human Genes and Gene Expression
; FILE REFERENCE: 2300-1480
; CURRENT APPLICATION NUMBER: US/10/076,555
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/217,471
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/068,755
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/080,664
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/105,234
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/105,877

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-27
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 218
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-076-555-218

Query Match 82.0%; Score 16.4; DB 14; Length 300;
Best Local Similarity 94.4%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGCTCTCTGAGTAGCAG 20

Db 222 GCGCTCTCTGAGTAGCAG 239

RESULT 12

US-10-076-555-842
; Sequence 842, Application US/10076555
; Publication No. US20030065156A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Lewis T.
; APPLICANT: Escobedo, Jaime
; APPLICANT: Innis, Michael A.
; APPLICANT: Garcia, Pablo Dominiguez
; APPLICANT: Sudduth-Klinger, Julie
; APPLICANT: Reinhard, Christoph
; APPLICANT: Giese, Klaus
; APPLICANT: Randazzo, Filippo
; APPLICANT: Kennedy, Giulia C.
; APPLICANT: Pot, David
; APPLICANT: Kassam, Altaf
; APPLICANT: Lamson, George
; APPLICANT: Drmanac, Radoje
; APPLICANT: Crkvenjakov, Radomir
; APPLICANT: Dickson, Mark
; APPLICANT: Drmanac, Snezana
; APPLICANT: Labat, Ivan
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Kita, David
; APPLICANT: Garcia, Veronica
; APPLICANT: Jones, Lee William
; APPLICANT: Stache-Crain, Birgit
; TITLE OF INVENTION: Novel Human Genes and Gene Expression
; FILE REFERENCE: 2300-1480
; CURRENT APPLICATION NUMBER: US/10/076,555
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/217,471
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/068,755
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/080,664
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/105,234
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/105,877
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 842
; LENGTH: 452
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(452)
; OTHER INFORMATION: n = A,T,C or G
US-10-076-555-842

Query Match 82.0%; Score 16.4; DB 14; Length 452;

```
Best Local Similarity 94.4%; Pred. No. 98;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGCTCTCTGAGTAGCAG 20
Db 222 GCGCTCTCTGAGCAGCAG 239

RESULT 13
US-10-260-238-3940/c
; Sequence 3940, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaiki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 3940
; LENGTH: 748
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-260-238-3940

Query Match 82.0%; Score 16.4; DB 17; Length 748;
Best Local Similarity 94.4%; Pred. No. 96;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGCTCTCTGAGTAGCAG 20
Db 235 GCGCTCTCCGAGTAGCAG 218

RESULT 14
US-10-104-047-1094
; Sequence 1094, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1094
; LENGTH: 1611
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-1094

Query Match 82.0%; Score 16.4; DB 17; Length 1611;
Best Local Similarity 94.4%; Pred. No. 92;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Best Local Similarity 94.4%; Pred. No. 98;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGCTCTCTGAGTAGCAG 20
Db 636 GCGCTCTCTGAGCAGCAG 653

RESULT 15
US-09-925-301-256
; Sequence 256, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 256
; LENGTH: 1992
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: {558}
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-301-256

Query Match 82.0%; Score 16.4; DB 9; Length 1992;
Best Local Similarity 94.4%; Pred. No. 91;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGCTCTCTGAGTAGCAG 20
Db 631 GCGCTCTCTGAGCAGCAG 648

RESULT 16
US-10-264-237-795/c
; Sequence 795, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131PI
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 795
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-264-237-795

Query Match 82.0%; Score 16.4; DB 17; Length 2665;
Best Local Similarity 94.4%; Pred. No. 90;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGCTCTCTGAGTAGCAG 20
Db 1169 GCGCTCTCTGAGCAGCAG 1152

RESULT 17
```



```
US-10-723-860-6203/c
; Sequence 6203, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Nataasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05982.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2003-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6203
; LENGTH: 4560
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-6203

Query Match      82.0%; Score 16.4; DB 18; Length 4560;
Best Local Similarity 94.4%; Pred. No. 87;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGCTCTCTGAGTAGCAG 20
|||||
Db 2727 GCGCTCTCTGAGTAGCAG 2710

RESULT 18
US-09-918-995-28588/c
; Sequence 28588, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28588
; LENGTH: 458
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(458)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-28588

Query Match      79.0%; Score 15.8; DB 10; Length 458;
Best Local Similarity 89.5%; Pred. No. 28+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGCTCTCTGAGTAGCA 19
|||||
Db 253 AGGGCGCTCTCTGAGTAGCA 235

RESULT 19
US-09-760-008A-2
; Sequence 2, Application US/09760008A
; Patent No. US20020004483A1
; GENERAL INFORMATION:
; APPLICANT: NISSEN, TORBEN LAUESGAARD
; APPLICANT: ANDERSEN, KIM VILBOUR
; APPLICANT: HANSEN, CHRISTIAN KARSTEN
US-09-760-008A-2

; APPLICANT: MIKKELSEN, JAN MOLLER
; TITLE OF INVENTION: G-CSF CONJUGATES
; FILE REFERENCE: 31-000700US
; CURRENT APPLICATION NUMBER: US/09/760,008A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/176,376
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/189,506
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/215,644
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DK PA 2000 00024
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: DK PA 2000 00341
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: DK PA 2000 00943
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-760-008A-2

Query Match      79.0%; Score 15.8; DB 9; Length 525;
Best Local Similarity 89.5%; Pred. No. 28+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGTCTCTGAGTAGCAG 20
|||||
Db 173 GGGCGCTCTGAGTAGCTG 191

RESULT 20
US-09-904-196B-2
; Sequence 2, Application US/09904196B
; Publication No. US20030064922A1
; GENERAL INFORMATION:
; APPLICANT: NISSEN, TORBEN LAUESGAARD
; APPLICANT: ANDERSEN, KIM VILBOUR
; APPLICANT: HANSEN, CHRISTIAN KARSTEN
; APPLICANT: MIKKELSEN, JAN MOLLER
; TITLE OF INVENTION: G-CSF CONJUGATES
; FILE REFERENCE: 31-000700US
; CURRENT APPLICATION NUMBER: US/09/904,196B
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US/09/760,008
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/176,376
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/189,506
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/215,644
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DK PA 2000 00024
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: DK PA 2000 00341
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: DK PA 2000 00943
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-904-196B-2
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; Query Match 79.0%; Score 15.8; DB 10; Length 525;
; Best Local Similarity 89.5%; Pred. No. 2e+02;
; Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGTCTCTGAGTAGCAG 20
Db 173 GGGCGCCTCTGAGTAGCTG 191

RESULT 21
US-10-192-294-2
; Sequence 2, Application US/10192294
; Publication No. US20030118612A1
; GENERAL INFORMATION:
; APPLICANT: NISSEN, Torben Lauesgaard
; TITLE OF INVENTION: G-CSF Conjugates
; FILE REFERENCE: 0258us310
; CURRENT APPLICATION NUMBER: US/10/192,294
; CURRENT FILING DATE: 2002-07-10
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: DK PA 2002 00447
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: DK PA 2002 00708
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: DNA sequence encoding hG-CSF, with codon usage for E. coli
US-10-192-294-2

Query Match 79.0%; Score 15.8; DB 15; Length 525;
; Best Local Similarity 89.5%; Pred. No. 2e+02;
; Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGTCTCTGAGTAGCAG 20
Db 173 GGGCGCCTCTGAGTAGCTG 191

RESULT 22
US-10-318-966-2
; Sequence 2, Application US/10318966
; Publication No. US20030158375A1
; GENERAL INFORMATION:
; APPLICANT: NISSEN, TORBEN LAUESGAARD
; APPLICANT: ANDERSEN, KIM VILBOUR
; APPLICANT: HANSEN, CHRISTIAN KARSTEN
; APPLICANT: MIKKELSEN, JAN MOLLER
; APPLICANT: SCHAMBYE, HANS THALSGARD
; TITLE OF INVENTION: G-CSF POLYPEPTIDES AND CONJUGATES
; FILE REFERENCE: 0208us620
; CURRENT APPLICATION NUMBER: US/10/318,966
; CURRENT FILING DATE: 2002-12-13
; PRIOR FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: 09/904,196
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/760,008
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/176,376
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/189,506
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/215,644
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DK PA 2000 00024
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: DK PA 2000 00024
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: DK PA 2000 00943
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-318-966-2

Query Match 79.0%; Score 15.8; DB 18; Length 525;
; Best Local Similarity 89.5%; Pred. No. 2e+02;
; Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGTCTCTGAGTAGCAG 20
Db 173 GGGCGCCTCTGAGTAGCTG 191

RESULT 24
US-10-003-496-5
; Sequence 5, Application US/10003496
; Publication No. US20020142964A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Aps
```

```
; PRIOR APPLICATION NUMBER: DK PA 2000 00943
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-318-966-2
```

```
Query Match 79.0%; Score 15.8; DB 16; Length 525;
; Best Local Similarity 89.5%; Pred. No. 2e+02;
; Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 GGGCGTCTCTGAGTAGCAG 20
Db 173 GGGCGCCTCTGAGTAGCTG 191
```

```
RESULT 23
US-10-705-745-2
; Sequence 2, Application US/10705745
; Publication No. US20040241806A1
; GENERAL INFORMATION:
; APPLICANT: NISSEN, TORBEN LAUESGAARD
; APPLICANT: ANDERSEN, KIM VILBOUR
; APPLICANT: HANSEN, CHRISTIAN KARSTEN
; APPLICANT: MIKKELSEN, JAN MOLLER
; TITLE OF INVENTION: G-CSF CONJUGATES
; FILE REFERENCE: 31-000700US
; CURRENT APPLICATION NUMBER: US/10/705,745
; CURRENT FILING DATE: 2003-11-10
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/176,376
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/189,506
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/215,644
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DK PA 2000 00024
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: DK PA 2000 00341
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: DK PA 2000 00943
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-705-745-2
```

```
Query Match 79.0%; Score 15.8; DB 18; Length 525;
; Best Local Similarity 89.5%; Pred. No. 2e+02;
; Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 GGGCGTCTCTGAGTAGCAG 20
Db 173 GGGCGCCTCTGAGTAGCTG 191
```

```
RESULT 24
US-10-003-496-5
; Sequence 5, Application US/10003496
; Publication No. US20020142964A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Aps
```

```
/ APPLICANT: Maxygen Holdings Ltd.
/ TITLE OF INVENTION: Single-Chain Polypeptides
/ FILE REFERENCE: 0218us210
/ CURRENT APPLICATION NUMBER: US/10/003,496
/ CURRENT FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: US 60/245,727
/ PRIOR FILING DATE: 2000-11-02
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 5
/ LENGTH: 531
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: DNA encoding G-CSF copy 2 in the single chain G-CSF dimer
US-10-003-496-5

Query Match          79.0%; Score 15.8; DB 13; Length 531;
Best Local Similarity 89.5%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GGGCGTCTCTGAGTAGCAG 20
Db      173 GGGCGCTCTGAGTAGCTG 191

RESULT 25
US-10-437-963-27903
/ Sequence 27903, Application US/10437963
/ Publication No. US20040123343A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Wu, Wei
/ APPLICANT: Boukharov, Andrey A.
/ APPLICANT: Barbazuk, Brad
/ APPLICANT: Li, Ping
/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53221)B
/ CURRENT APPLICATION NUMBER: US/10/437,963
/ CURRENT FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 27903
/ LENGTH: 600
/ TYPE: DNA
/ ORGANISM: Oryza sativa
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_32553C.1
US-10-437-963-27903

Query Match          79.0%; Score 15.8; DB 18; Length 600;
Best Local Similarity 89.5%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 AGGGCGTCTCTGAGTAGCA 19
Db      249 AGGGCGTCTCTGAGGAGCA 267

RESULT 26
US-10-027-632-142002
/ Sequence 142002, Application US/10027632
/ Publication No. US20020198371A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ TITLE OF INVENTION: Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ CURRENT FILING DATE: 2002-04-30
```

```
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 142002
/ LENGTH: 874
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-142002

Query Match          79.0%; Score 15.8; DB 13; Length 874;
Best Local Similarity 89.5%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GGGCGTCTCTGAGTAGCAG 20
Db      402 GGGCGCTCTGAGTAGTACAG 420

RESULT 27
US-10-027-632-169596
/ Sequence 169596, Application US/10027632
/ Publication No. US20020198371A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ TITLE OF INVENTION: Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ CURRENT FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 169596
/ LENGTH: 874
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-169596

Query Match          79.0%; Score 15.8; DB 13; Length 874;
Best Local Similarity 89.5%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GGGCGTCTCTGAGTAGCAG 20
Db      402 GGGCGCTCTGAGTAGTACAG 420
```

RESULT 28
US-10-027-632-142002
; Sequence 142002, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142002
; LENGTH: 874
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-142002

Query Match 79.0%; Score 15.8; DB 17; Length 874;
Best Local Similarity 89.5%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGCTCTGAGTAGCAG 20
||||| ||||| ||||| ||||| |||||
Db 402 GGGCGCTCTGAGTAGCAG 420

RESULT 29
US-10-027-632-169596
; Sequence 169596, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 169596
; LENGTH: 874
; TYPE: DNA
; ORGANISM: Human

Query Match 79.0%; Score 15.8; DB 17; Length 874;
Best Local Similarity 89.5%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGCTCTGAGTAGCAG 20
||||| ||||| ||||| ||||| |||||
Db 402 GGGCGCTCTGAGTAGCAG 420

US-10-027-632-169596

Query Match 79.0%; Score 15.8; DB 17; Length 874;
Best Local Similarity 89.5%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGCTCTGAGTAGCAG 20
||||| ||||| ||||| ||||| |||||
Db 402 GGGCGCTCTGAGTAGCAG 420

RESULT 30
US-10-027-632-116504/c
; Sequence 116504, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 116504
; LENGTH: 1113
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-116504

Query Match 79.0%; Score 15.8; DB 13; Length 1113;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGCGCTCTGAGTAGCA 19
||||| ||||| ||||| ||||| |||||
Db 279 AGGGCGCTCTGAGGAGCA 261

RESULT 31
US-10-027-632-116504/c
; Sequence 116504, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 116504
; LENGTH: 1113
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-116504

Query Match 79.0%; Score 15.8; DB 17; Length 1113;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGCGCTCTCTGAGTAGCA 19
||||| ||||| ||||| |||||
Db 279 AGGCGCTCTCTGAGGACCA 261

RESULT 32
US-10-424-599-16815/c
; Sequence 16815, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 16815
; LENGTH: 1196
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_11518C.1
US-10-424-599-16815

Query Match 79.0%; Score 15.8; DB 17; Length 1196;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGTCTCTGAGTAGCAG 20
||||| ||||| ||||| |||||
Db 401 GGGCGTCTCGGAGTAGCTG 383

RESULT 33
US-10-437-963-34349/c
; Sequence 34349, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 34349
; LENGTH: 1326
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_38372C.1
US-10-437-963-34349

Query Match 79.0%; Score 15.8; DB 18; Length 1326;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGTCTCTGAGTAGCAG 20
||||| ||||| ||||| |||||
Db 304 GGGCTTCTCTGAGTATCAG 286

RESULT 34
US-10-424-599-110517
; Sequence 110517, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 110517
; LENGTH: 1938
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_70808C.1
US-10-424-599-110517

Query Match 79.0%; Score 15.8; DB 17; Length 1938;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGTCTCTGAGTAGCAG 20
||||| ||||| ||||| |||||
Db 1040 GGGCGTCTCTAGTTGCAG 1058

RESULT 35
US-10-437-963-67253/c
; Sequence 67253, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 67253
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_68127C.1
US-10-437-963-67253

Query Match 79.0%; Score 15.8; DB 18; Length 2196;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGGCGTCTCTGAGTAGCA 19
||||| ||||| ||||| |||||
Db 2061 AGGCGATCTCTGAGAGCA 2043

RESULT 36

US-10-027-632-111979/c
; Sequence 111979, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 111979

; LENGTH: 2597

; TYPE: DNA

; ORGANISM: Human

US-10-027-632-111979

Query Match 79.0%; Score 15.8; DB 13; Length 2597;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGCGTCTCTGAGTAGCAG 20
||||| ||||| ||||| |||||
Db 2018 GGGCGTTTCTGAGGAGCAG 2000

RESULT 37

US-10-027-632-111979/c
; Sequence 111979, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 111979
; LENGTH: 2597
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-111979

Query Match 79.0%; Score 15.8; DB 17; Length 2597;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGCGTCTCTGAGTAGCAG 20
||||| ||||| ||||| |||||
Db 2018 GGGCGTTTCTGAGGAGCAG 2000

RESULT 38

US-10-160-865-15/c

; Sequence 15, Application US/10160865

; Publication No. US20020169139A1

; GENERAL INFORMATION:

; APPLICANT: Lee, Mu-En

; APPLICANT: Hsieh, Chung-Ming

; TITLE OF INVENTION: SINGLE GENE ENCODING AORTIC-SPECIFIC AND STRIATED-SPECIFIC
MUSCLE CELL ISOFORMS AND USES THEREOF

; FILE REFERENCE: 05433/038001

; CURRENT APPLICATION NUMBER: US/10/160,865

; CURRENT FILING DATE: 2002-06-03

; PRIOR APPLICATION NUMBER: US/09/134,250

; PRIOR FILING DATE: 1998-08-14

; PRIOR APPLICATION NUMBER: US 08/795,868

; PRIOR FILING DATE: 1997-02-06

; PRIOR APPLICATION NUMBER: US 08/494,577

; PRIOR FILING DATE: 1995-06-22

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 15

; LENGTH: 2614

; TYPE: DNA

; ORGANISM: Mus musculus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(1806)

US-10-160-865-15

Query Match 79.0%; Score 15.8; DB 13; Length 2614;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGCGTCTCTGAGTAGCAG 20
||||| ||||| ||||| |||||
Db 1273 GGGCGTCTCTGAGGAGCAG 1255

RESULT 39

US-09-791-105-1/c

; Sequence 1, Application US/09791105

; Patent No. US200202225A1

; GENERAL INFORMATION:

; APPLICANT: Epidauros Biotechnologie AG

; TITLE OF INVENTION: Method for detecting the presence of at least one single allele of

; a deletion mutant

; FILE REFERENCE: EPI 01/00

; CURRENT APPLICATION NUMBER: US/09/791,105

; CURRENT FILING DATE: 2001-02-22

; PRIOR APPLICATION NUMBER: EP 00103844.7

<p>Qy 2 GGGCGTCTCTGAGTAGCAG 20 Db 3918 GGGCGTCTCTGAGTAGGAG 3900</p> <p>RESULT 42</p> <p>US-10-491-566-87/c ; Sequence 87, Application US/10491566 ; Publication No. US20040249144A1 ; GENERAL INFORMATION: ; APPLICANT: Origene Technologies Inc ; TITLE OF INVENTION: Regulated Breast Cancer Genes ; FILE REFERENCE: 3U 103 R1 ; CURRENT APPLICATION NUMBER: US/10/491,566 ; CURRENT FILING DATE: 2004-04-05 ; NUMBER OF SEQ ID NOS: 148 ; SOFTWARE: PatentIn version 3.1 ; SEQ ID NO 87 ; LENGTH: 5866 ; TYPE: DNA ; ORGANISM: Homo sapiens ; FEATURE: ; NAME/KEY: CDS ; LOCATION: (1)..(5721) ; OTHER INFORMATION: US-10-491-566-87</p>	<p>Query Match 79.0%; Score 15.8; DB 18; Length 5866; Best Local Similarity 89.5%; Pred. No. 1.8e+02; Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;</p>
<p>Qy 2 GGGCGTCTCTGAGTAGCAG 20 Db 3918 GGGCGTCTCTGAGTAGGAG 3900</p> <p>RESULT 43</p> <p>US-09-997-722-124/c ; Sequence 124, Application US/09997722 ; Publication No. US20040072154A1 ; GENERAL INFORMATION: ; APPLICANT: Morris, David ; APPLICANT: Engelhard, Eric ; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER ; FILE REFERENCE: A-71171/RMS/DCF ; CURRENT APPLICATION NUMBER: US/09/997,722 ; CURRENT FILING DATE: 2001-11-30 ; PRIOR APPLICATION NUMBER: US 09/747,377 ; PRIOR FILING DATE: 2000-12-22 ; PRIOR APPLICATION NUMBER: US 09/798,586 ; PRIOR FILING DATE: 2001-03-02 ; NUMBER OF SEQ ID NOS: 301 ; SOFTWARE: PatentIn version 3.1 ; SEQ ID NO 124 ; LENGTH: 53795 ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-997-722-124</p>	<p>Query Match 79.0%; Score 15.8; DB 11; Length 53795; Best Local Similarity 89.5%; Pred. No. 1.6e+02; Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;</p>
<p>Qy 2 GGGCGTCTCTGAGTAGCAG 20 Db 21159 GGGCGTCTCTGATGACGAG 21141</p> <p>RESULT 44</p> <p>US-10-450-826-68/c ; Sequence 68, Application US/10450826 ; Publication No. US20040101818A1 ; GENERAL INFORMATION:</p>	<p>Query Match 79.0%; Score 15.8; DB 17; Length 5866; Best Local Similarity 89.5%; Pred. No. 1.8e+02; Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;</p>

[illegible]

<p>Qy 2 GGGCGTCTCTGAGTAGCAG 20 Db 3918 GGGCGTCTCGGAGTAGGAG 3900</p> <p>RESULT 42</p> <p>US-10-491-566-87/c ; Sequence 87, Application US/10491566 ; Publication No. US20040249144A1 ; GENERAL INFORMATION: ; APPLICANT: Origene Technologies Inc ; TITLE OF INVENTION: Regulated Breast Cancer Genes ; FILE REFERENCE: 3U 103 R1 ; CURRENT APPLICATION NUMBER: US/10/491,566 ; CURRENT FILING DATE: 2004-04-05 ; NUMBER OF SEQ ID NOS: 148 ; SOFTWARE: PatentIn version 3.1 ; SEQ ID NO 87 ; LENGTH: 5866 ; TYPE: DNA ; ORGANISM: Homo sapiens ; FEATURE: ; NAME/KEY: CDS ; LOCATION: (1)..(5721) ; OTHER INFORMATION: US-10-491-566-87</p>	<p>Query Match 79.0%; Score 15.8; DB 18; Length 5866; Best Local Similarity 89.5%; Pred. No. 1.8e+02; Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;</p>
<p>Qy 2 GGGCGTCTCTGAGTAGCAG 20 Db 3918 GGGCGTCTCGGAGTAGGAG 3900</p> <p>RESULT 43</p> <p>US-09-997-722-124/c ; Sequence 124, Application US/09997722 ; Publication No. US20040072154A1 ; GENERAL INFORMATION: ; APPLICANT: Morris, David ; APPLICANT: Engelhard, Eric ; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER ; FILE REFERENCE: A-71171/RMS/DCF ; CURRENT APPLICATION NUMBER: US/09/997,722 ; CURRENT FILING DATE: 2001-11-30 ; PRIOR APPLICATION NUMBER: US 09/747,377 ; PRIOR FILING DATE: 2000-12-22 ; PRIOR APPLICATION NUMBER: US 09/798,586 ; PRIOR FILING DATE: 2001-03-02 ; NUMBER OF SEQ ID NOS: 301 ; SOFTWARE: PatentIn version 3.1 ; SEQ ID NO 124 ; LENGTH: 53795 ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-997-722-124</p>	<p>Query Match 79.0%; Score 15.8; DB 11; Length 53795; Best Local Similarity 89.5%; Pred. No. 1.6e+02; Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;</p>
<p>Qy 2 GGGCGTCTCTGAGTAGCAG 20 Db 21159 GGGCGTCTGTATGAGCAG 21141</p> <p>RESULT 44</p> <p>US-10-450-826-68/c ; Sequence 68, Application US/10450826 ; Publication No. US20040101818A1 ; GENERAL INFORMATION:</p>	<p>Query Match 79.0%; Score 15.8; DB 17; Length 5866; Best Local Similarity 89.5%; Pred. No. 1.8e+02; Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;</p>

```

; APPLICANT: Ji, Darren
; APPLICANT: Axelrod, Douglas W.
; APPLICANT: Cook, Jonathan S.
; APPLICANT: Jaiswal, Neelam
; APPLICANT: Bistein, Richard
; APPLICANT: Houghton, Adam
; APPLICANT: Mertz, Lawrence
; TITLE OF INVENTION: Gene Expression Profiles Associated with Osteoblast Differentiation
; FILE REFERENCE: 044921-5039-WO
; CURRENT APPLICATION NUMBER: US/10/450,826
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 60/255,882
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/285,691
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
; LENGTH: 73465
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. AL109748
US-10-450-826-68

Query Match          79.0%; Score 15.8; DB 18; Length 73465;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2  GGGCGTCTCTGAGTAGCAG 20
Db   23585 GAGCGTCTGTGAGTAGCAG 23567

RESULT 45
US-10-148-806-3
; Sequence 3, Application US/10148806
; Publication No. US20030138933A1
; GENERAL INFORMATION:
; APPLICANT: Bai, Chang
; APPLICANT: Metzger, Michael
; APPLICANT: Liu, Xiaomei
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NHL, A DNA
; FILE REFERENCE: 20585P
; CURRENT APPLICATION NUMBER: US/10/148,806
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US00/33065
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: 60/169,970
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 114793
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-148-806-3

Query Match          79.0%; Score 15.8; DB 15; Length 114793;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2  GGGCGTCTCTGAGTAGCAG 20
Db   49994 GGGCCTCTCTGAGGACGAG 50012

RESULT 46
US-10-723-860-199
; Sequence 199, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlocnik, Albert
; TITLE OF INVENTION: Methods of diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 199
; LENGTH: 153170
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-199

Query Match          79.0%; Score 15.8; DB 18; Length 153170;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  1  AGGGCGTCTCTGAGTAGCA 19
Db   119585 AGGGCCTCTCTGAGGACGA 119603

RESULT 47
US-10-425-115-71771
; Sequence 71771, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 71771
; LENGTH: 397
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_165459C.1
US-10-425-115-71771

Query Match          77.0%; Score 15.4; DB 18; Length 397;
Best Local Similarity 94.1%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1  AGGGCGTCTCTGAGTAG 17
Db   4  AGGGCGTCCCTGAGTAG 20

RESULT 48
US-10-653-047-1507/c
; Sequence 1507, Application US/10653047
; Publication No. US20040229367A1
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 5849.200-US
```

```

; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlocnik, Albert
; TITLE OF INVENTION: Methods of diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 199
; LENGTH: 153170
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-199

Query Match          79.0%; Score 15.8; DB 18; Length 153170;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  1  AGGGCGTCTCTGAGTAGCA 19
Db   119585 AGGGCCTCTCTGAGGACGA 119603

RESULT 47
US-10-425-115-71771
; Sequence 71771, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 71771
; LENGTH: 397
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_165459C.1
US-10-425-115-71771

Query Match          77.0%; Score 15.4; DB 18; Length 397;
Best Local Similarity 94.1%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1  AGGGCGTCTCTGAGTAG 17
Db   4  AGGGCGTCCCTGAGTAG 20

RESULT 48
US-10-653-047-1507/c
; Sequence 1507, Application US/10653047
; Publication No. US20040229367A1
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 5849.200-US
```


; CURRENT APPLICATION NUMBER: US/10/653,047
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/533,559
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/273,623
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1507
; LENGTH: 431
; TYPE: DNA
; ORGANISM: Fusarium venenatum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(431)
; OTHER INFORMATION: n = A,T,C or G
US-10-653-047-1507

Query Match 77.0%; Score 15.4; DB 18; Length 431;
Best Local Similarity 94.1%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGCGTCTCTGAGTAGC 18
Db 103 GGGCGTATCTGAGTAGC 87

RESULT 49

US-09-560-863-242
; Sequence 242, Application US/09560863
; Patent No. US20020110809A1
; GENERAL INFORMATION:
; APPLICANT: Nehls, Michael C.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.

; TITLE OF INVENTION: No. US20020110809A1el Human Polynucleotides and the
; FILE REFERENCE: LEX-0018-USA

; CURRENT APPLICATION NUMBER: US/09/560,863
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/132,408
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 1008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 242
; LENGTH: 433
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(433)
; OTHER INFORMATION: n = A,T,C or G

US-09-560-863-242

Query Match 77.0%; Score 15.4; DB 9; Length 433;
Best Local Similarity 94.1%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GCGTCTCTGAGTAGCAG 20
Db 59 GCCTCTCTGAGTAGCAG 75

RESULT 50

US-09-783-590-10350/c
; Sequence 10350, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:

; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.

; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16.2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10350
; LENGTH: 488
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (122)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (137)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (188)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (252)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (272)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (314)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (330)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (337)
; OTHER INFORMATION: n equals a,t,g, or c
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; LOCATION: (340)
; OTHER INFORMATION: n equals a,t,g, or c
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; LOCATION: (351)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (354)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (363)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (372)
; OTHER INFORMATION: n equals a,t,g, or c
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; LOCATION: (386)
; OTHER INFORMATION: n equals a,t,g, or c
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; LOCATION: (394)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (419)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (423)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (426)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature

; LOCATION: (431)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (434)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (440)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (459)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (464)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-10350

Query Match 77.0%; Score 15.4; DB 9; Length 488;
Best Local Similarity 94.1%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGCGTCTCTGAGTAGC 18
| | | | | | | | | | | | | | | | | |
Db 72 GGGCGTCTCTGAGTAGC 56

Search completed: March 15, 2005, 00:22:50
Job time : 365 secs